

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 22:17:57 ; Search time 1535 Seconds

(without alignments)  
564.730 Million cell updates/sec

Title: US-09-693-205A-47

Perfect score: 20

Sequence: 1 gtgaatggccacttgcact 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 1036652

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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4: gb\_om: \*  
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14: gb\_vl: \*  
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16: em\_fun: \*  
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30: em\_hcg\_hum: \*  
31: em\_hcg\_inv: \*  
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37: em\_hcg\_vrt: \*  
38: em\_sy: \*  
39: em\_hcgo\_hum: \*  
40: em\_hcgo\_mus: \*  
41: em\_hcgo\_other: \*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13.2	66.0	24	6 AX290535	AX290535 Sequence
C 2	13	65.0	20	6 AR437040	AR437040 Sequence
C 3	13	65.0	21	6 AX154399	AX154399 Sequence
C 4	12.6	63.0	21	6 BD167262	BD167262 Human 11v
C 5	12.4	62.0	20	6 AR100612	AR100612 Sequence
C 6	12.4	62.0	20	6 AR121611	AR121611 Sequence
C 7	12.4	62.0	20	6 AR311314	AR311314 Sequence
C 8	12.4	62.0	24	6 AX447358	AX447358 Sequence
C 9	12.2	61.0	17	6 AR142556	AR142556 Sequence
C 10	12.2	61.0	17	6 AR142558	AR142558 Sequence
C 11	12.2	61.0	17	6 E49149	E49149 Cocci-diosis
C 12	12.2	61.0	17	6 E49151	E49151 Cocci-diosis
C 13	12	60.0	23	6 AX365154	AX365154 Sequence
C 14	11.8	59.0	19	6 BD089690	BD089690 A method
C 15	11.8	59.0	19	12 AB068455	AB068455 Synthetic
C 16	11.8	59.0	21	6 AR212666	AR212666 Sequence
C 17	11.6	58.0	19	6 AX082100	AX082100 Sequence
C 18	11.6	58.0	19	6 AX082100	AX082100 Sequence
C 19	11.6	58.0	20	6 AX316266	AX316266 Sequence
C 20	11.6	58.0	24	6 BD179353	BD179353 Insulin-1
C 21	11.6	58.0	24	6 BD179354	BD179354 Insulin-1
C 22	11.6	58.0	24	9 HUMXP587B	L32074 Homo sapien
C 23	11.6	58.0	25	6 AX609328	AX609328 Sequence
C 24	11.4	57.0	17	6 BD254521	BD254521 Regulatio
C 25	11.4	57.0	17	6 AX758367	AX758367 Sequence
C 26	11.4	57.0	19	6 BD266251	BD266251 Universal
C 27	11.4	57.0	20	6 BD243093	BD243093 Antisense
C 28	11.4	57.0	20	6 BD243094	BD243094 Antisense
C 29	11.4	57.0	20	6 BD243095	BD243095 Antisense
C 30	11.4	57.0	20	6 BD243096	BD243096 Antisense
C 31	11.4	57.0	20	6 AX189426	AX189426 Sequence
C 32	11.4	57.0	20	6 AX189430	AX189430 Sequence
C 33	11.4	57.0	20	6 AX295168	AX295168 Sequence
C 34	11.4	57.0	21	6 AR083899	AR083899 Sequence
C 35	11.4	57.0	21	6 AR278835	AR278835 Sequence
C 36	11.4	57.0	21	6 AX095410	AX095410 Sequence
C 37	11.4	57.0	21	6 AX095574	AX095574 Sequence
C 38	11.4	57.0	23	6 AR063162	AR063162 Sequence
C 39	11.4	57.0	23	6 AR071358	AR071358 Sequence
C 40	11.4	57.0	23	6 AR119344	AR119344 Sequence
C 41	11.4	57.0	23	6 AX384685	AX384685 Sequence
C 42	11.4	57.0	24	6 A63197	A63197 Sequence 11
C 43	11.4	57.0	24	6 AX443656	AX443656 Sequence
C 44	11.4	57.0	25	6 AX447638	AX447638 Sequence
C 45	11.2	56.0	17	6 AX579610	AX579610 Sequence

#### ALIGNMENTS

RESULT 1  
AX290535/c  
LOCUS AX290535 24 bp DNA  
DEFINITION Sequence 2297 from Patent WO0179548.  
ACCESSION AX290535  
VERSION AX290535.1 GI:17052218  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1  
Baranyi,F., Zilvi,M., Gerry,N.P., Pavls,R. and Kilman,R.  
Method of designing addressable array for detection of nucleic acid  
sequence differences using ligase detection reaction  
JOURNAL Patent: WO 0179548-A 2297 25-OCT-2001;



QY 7 GGCCACTTGGCACT 20  
 Db 16 GGCCACTTGGCACT 3

RESULT 6  
 LOCUS AR121611/c 20 bp DNA  
 DEFINITION Sequence 8 from patent US 6159946.  
 ACCESSION AR121611  
 VERSION AR121611.1 GI:14105187  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Zaleski,A. and Shi,Y.  
 TITLE Antisense inhibition of c-myc to modulate the proliferation of smooth muscle cells  
 JOURNAL Patent: US 6159946-A 8 12-DEC-2000;  
 FEATURES Location/Qualifiers  
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 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGCCACTTGGCACT 20  
 Db 16 GGCCACTTGGCACT 3

RESULT 7  
 LOCUS AR311314 20 bp DNA  
 DEFINITION Sequence 1851 from patent US 6559294.  
 ACCESSION AR311314  
 VERSION AR311314.1 GI:31704740  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Grifflats,R., Holseth,S.X., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Fletcher,L.D.  
 TITLE Chlamydia pneumoniae polynucleotides and uses thereof  
 JOURNAL Patent: US 6559294-A 1851 06-MAY-2003;  
 FEATURES Location/Qualifiers  
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QY 7 GGCCACTTGGCACT 20  
 Db 2 GGCCACTTGGCACT 15

RESULT 8  
 LOCUS AX447358 24 bp DNA  
 DEFINITION Sequence 3813 from Patent WO0216649.  
 ACCESSION AX447358  
 VERSION AX447358.1 GI:21696257  
 KEYWORDS

SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.

REFERENCE 1  
 AUTHORS Gunderson,K.  
 TITLE Probes and decoder oligonucleotides  
 JOURNAL Patent: WO 0216649-A 3813 28-FEB-2002;  
 FEATURES Illumina, Inc. (US)  
 source 1..24  
 Location/Qualifiers  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Computer Generated Probe Sequence."

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 Best Local Similarity 92.9%; Pred.No.1.1e+05;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GAATGGCCACTTGG 16  
 Db 23 GAATGGCCACTTGG 10

RESULT 9  
 LOCUS AR142556 17 bp DNA  
 DEFINITION Sequence 15 from patent US 6203801.  
 ACCESSION AR142556  
 VERSION AR142556.1 GI:15103842  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)  
 AUTHORS Schaad,T.Cornelis., Kuiper,C.Maria. and Vermeulen,A.Nicolaas.  
 TITLE Coccidioides polypeptide and vaccines  
 JOURNAL Patent: US 6203801-A 15 20-MAR-2001;  
 FEATURES Location/Qualifiers  
 source 1..17  
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 /mol\_type="unassigned DNA"

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QY 1 GTGATGGCCACTTGG 17  
 Db 1 GTGATGGCCACTTGG 17

RESULT 10  
 LOCUS AR142558 17 bp DNA  
 DEFINITION Sequence 17 from patent US 6203801.  
 ACCESSION AR142558  
 VERSION AR142558.1 GI:15103844  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)  
 AUTHORS Schaad,T.Cornelis., Kuiper,C.Maria. and Vermeulen,A.Nicolaas.  
 TITLE Coccidioides polypeptide and vaccines  
 JOURNAL Patent: US 6203801-A 17 20-MAR-2001;  
 FEATURES Location/Qualifiers  
 source 1..17  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

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Best Local Similarity 82.4%; Pred. No. 1.4e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGGCCACTTTGC 17  
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1 GTGAATGGGACTTTGC 17

Db

RESULT 11

LOCUS E49149 17 bp DNA linear PAT 31-JAN-2002

DEFINITION Coccidioides vaccine.

ACCESSION E49149

VERSION E49149.1 GI:18629274

KEYWORDS JP 2000219635-A/9.

SOURCE unclassified

ORGANISM unclassified

REFERENCE 1 (bases 1 to 17)  
Schaepe,T.C., Kalberu,K.M. and Fuertumuren,A.N.  
Coccidioides vaccine  
Patent: JP 2000219635-A 9 08-AUG-2000;  
AKZO NOBEL NV

COMMENT OS Unidentified  
PN JP 2000219635-A/9  
PD 08-AUG-2000  
PF 01-OCT-1999 JP 1999281680  
PR 07-OCT-1998 EP 98203384.7,16-OCT-1998 EP 98203457.1 PI  
THEODORUS CORNELISZ SCHAEPE,KATARINA MARIA KAIBERU, PI ALNOLODUS  
NICHOLAS FUERTUMUREN

PC A61K39/00,A61K39/012,A61K39/108,A61K39/112,A61K39/15,A61K39/17, PC  
A61K39/21,  
PC A61K39/215,A61K39/235,A61K39/255,A61K39/39,A61P33/02, PC  
C07K14/455,C12N15/09,  
PC G01N33/569,C12N15/00  
CC Strandedness: Double;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..17  
Location/Qualifiers  
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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGGCCACTTTGC 17  
|||||  
1 GTGAATGGGACTTTGC 17

Db

RESULT 12

LOCUS E49151 17 bp DNA linear PAT 31-JAN-2002

DEFINITION Coccidioides vaccine.

ACCESSION E49151

VERSION E49151.1 GI:18629276

KEYWORDS JP 2000219635-A/11.

SOURCE unclassified

ORGANISM unclassified

REFERENCE 1 (bases 1 to 17)  
Schaepe,T.C., Kalberu,K.M. and Fuertumuren,A.N.  
Coccidioides vaccine  
Patent: JP 2000219635-A 11 08-AUG-2000;  
AKZO NOBEL NV

COMMENT AKZO NOBEL NV  
OS Unidentified  
PN JP 2000219635-A/11  
PD 08-AUG-2000  
PF 01-OCT-1999 JP 1999281680  
PR 07-OCT-1998 EP 98203384.7,16-OCT-1998 EP 98203457.1 PI  
THEODORUS CORNELISZ SCHAEPE,KATARINA MARIA KAIBERU, PI ALNOLODUS  
NICHOLAS FUERTUMUREN

PC A61K39/00,A61K39/012,A61K39/108,A61K39/112,A61K39/15,A61K39/17, PC  
A61K39/21,  
PC A61K39/215,A61K39/235,A61K39/255,A61K39/39,A61P33/02, PC  
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PC G01N33/569,C12N15/00  
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CC Topology: Linear;  
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FEATURES  
source

ORIGIN

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Best Local Similarity 82.4%; Pred. No. 1.4e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGGCCACTTTGC 17  
|||||  
1 GTGAATGGGACTTTGC 17

Db

RESULT 13

LOCUS AX365154/c 23 bp DNA linear PAT 15-FEB-2002

DEFINITION Sequence 6 from Patent WO0200721.

ACCESSION AX365154

VERSION AX365154.1 GI:18696912

KEYWORDS

SOURCE synthetic construct  
synthetic construct  
artificial sequences.

ORGANISM

REFERENCE 1  
Sprecher,C.A., Presnell,S.R., Gao,Z., Whitmore,T.E., Kuiper,J.L.  
and Maurer,M.F.  
Cytokine receptor zcytor17  
Patent: WO 0200721-A 6 03-JAN-2002;  
ZymoGenetics, Inc. (US)  
Location/Qualifiers  
1..23  
/organism='synthetic construct'  
/mol\_type='unassigned DNA'  
/db\_xref='taxon:32630'  
/note='Oligonucleotide primer zc27898'

ORIGIN

Query Match 60.0%; Score 12; DB 6; Length 23;  
Best Local Similarity 75.0%; Pred. No. 1.8e+05;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTGAATGGCCACTTTGACT 20  
|||||  
22 GTGATGAGCTGCTCTGCGCT 3

Db

RESULT 14

LOCUS BD089690/c 19 bp DNA linear PAT 27-AUG-2002

DEFINITION A method of arraying genome clone.

ACCESSION BD089690



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VERSION BD089690.1 GI:22635300  
KEYWORDS JP 2001321190-A/1934.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Soeda,E.  
TITLE A method of arraying genome clone  
JOURNAL Patent: JP 2001321190-A 1934 20-NOV-2001;  
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKATSHA  
COMMENT  
GENOTCHS OS Artificial Sequence  
PN JP 2001321190-A/1934  
PD 20-NOV-2001  
PF 12-MAR-2001 JP 2001068285  
PI EIICHI SOEDA  
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC  
C12N15/00  
PC C12N15/00  
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Best Local Similarity 86.7%; Pred.No.2.3e+05;  
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DB 16 TGCCCACTGAGCACT 2  
RESULT 15  
AB068455 19 bp DNA linear SYN 21-MAY-2003  
LOCUS AB068455/c  
DEFINITION Synthetic construct DNA, reverse primer for human STS sts-cos26-T7  
at 1p36.  
ACCESSION AB068455  
VERSION AB068455.1 GI:15129259  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
1  
synthetic construct  
synthetic construct  
artificial sequences.  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
A BAC-based STS-content map spanning a 35-Mb region of human  
chromosome 1p35-p36  
Genomics 74 (1), 55-70 (2001)  
21269192  
MEDLINE  
11374902  
PUBMED  
2 (bases 1 to 19)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Direct Submission  
Submitted (04-AUG-2001) Akira Horii, Tohoku University School of  
Medicine, Molecular Pathology, 2-1 Seiryomachi, Aoba-ku, Sendai,  
Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,  
tel:81-22-717-8042, Fax:81-22-717-8047)  
FEATURES  
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/db\_xref="taxon:32630"  
misc\_feature 1..19

/note="reverse primer for human STS sts-cos26-T7 at 1p36  
sts-cos26-T7 obtained from clones B307023, B191E13,  
B191F10, B192B7, B192K5, B2806, B31F10, B382616, B307020,  
Human BAC library RPCI-11"  
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Query Match 59.0%; Score 11.8; DB 12; Length 19;  
Best Local Similarity 86.7%; Pred.No.2.3e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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DB 16 TGCCCACTGAGCACT 2  
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Job time : 1537 secs

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 22:14:37 ; Search time 331 seconds  
(without alignments)  
256.689 Million cell updates/sec

Title: US-09-693-205A-47  
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Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124093041 residues

Total number of hits satisfying chosen parameters: 2488994

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Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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10: geneseqn2004as:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
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7	12.8	64.0	21	ADD15186	Add15186 Reverse P
8	12.8	64.0	21	ACH54316	Ach54316 DNA targ
9	12.6	63.0	21	ABV84997	Abv84997 Human galy
10	12.6	63.0	25	ACI25331	Ac125331 Human mlt
11	12.6	63.0	25	ACI94288	Ac194288 Human mlt
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16	12.4	62.0	20	AAQ70717	Aaq70717 C-myc gen
17	12.2	61.0	17	AAZ94912	Aaz94912 Elmeria t
18	12.2	61.0	17	AAZ94910	Aaz94910 Elmeria t
19	12.2	61.0	18	AAF25719	Aaf25719 C. purpur
20	12.2	61.0	23	AAZ62464	Aaz62464 Baxley th
21	12.2	61.0	23	AAZ62464	Aaz62464 Baxley th
22	12.2	61.0	23	AAZ62464	Aaz62464 Baxley th
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C	26	11.8	59.0	19	6	ABL44890	Ab144890 Human chr
C	27	11.8	59.0	21	2	AAV84146	Aav84146 Human pro
C	28	11.8	59.0	21	4	AAE95987	Aae95987 Human gen
C	29	11.8	59.0	21	4	AAH62596	Aah62596 CHRNA7 po
C	30	11.8	59.0	22	2	AAV00577	Aav00577 PCR prime
C	31	11.8	59.0	22	7	ADA05959	Ada05959 Human NOV
C	32	11.8	59.0	25	3	AAZ58093	Aaz58093 Human PRO
C	33	11.8	59.0	25	8	ACH59115	Ach59115 DNA targ
C	34	11.6	58.0	19	4	AAE91257	Aae91257 Human mul
C	35	11.6	58.0	19	4	AAE91255	Aae91255 Human mul
C	36	11.6	58.0	20	6	ABK24579	Abk24579 EIF2AK3 c
C	37	11.6	58.0	21	9	ADH86760	Adh86760 M-CSF-R p
C	38	11.6	58.0	24	7	ABZ21752	Abz21752 Human IGF
C	39	11.6	58.0	24	7	ABZ21753	Abz21753 Human IGF
C	40	11.6	58.0	25	8	ACI76320	Ac176320 Human mlt
C	41	11.6	58.0	25	8	ACI76321	Ac176321 Human mlt
C	42	11.6	58.0	25	8	ACT80229	Act80229 Human mlt
C	43	11.6	58.0	25	8	ACT80229	Act80229 Human mlt
C	44	11.4	57.0	15	4	AAF52168	Aaf52168 IGF-I o11
C	45	11.4	57.0	15	4	AAF52167	Aaf52167 IGF-I o11

#### ALIGNMENTS

RESULT 1  
AAH20154  
ID AAH20154 standard; DNA; 20 BP.  
XX  
AC AAH20154;  
XX  
DT 09-AUG-2001 (first entry)  
XX  
DE Human spactin CRF PCR primer SEQ ID NO:47.  
XX  
KW Human; mouse; spactin; ARSACS; chromosome 13q11; identification;  
KW autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation;  
KW neurodegenerative disease; reduced sensory nerve conduction; diagnosis;  
KW reduced motor nerve velocity; hypermyelination of retinal nerve fibre;  
KW atrophy of upper cerebellar vermis; absence of Purkinje cell;  
KW abnormal neuronal lipid storage; genetic disorder; characterisation;  
KW PCR primer; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
OS  
PN WO200129266-A2.  
XX  
PD 26-APR-2001.  
XX  
PF 20-OCT-2000; 2000WO-US029130.  
XX  
PR 20-OCT-1999; 99US-0160588P.  
XX  
PA (UWMC-) UNIV MCGILL.  
PA (HOPI-) HOPITAL SAINTE-JUSTINE.  
XX  
PI Hudson TJ, Engert J, Richter A;  
XX  
DR WPI; 2001-308494/32.  
XX  
PT New isolated polymucleotide, encoding spactin gene, and polypeptides,  
PT useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-  
PT Saguenay disease by detecting two point mutations in spactin gene  
PT sequence.  
XX  
PS Claim 23; Fig 7; 76pp; English.  
XX  
CC The present invention describes human and mouse spactin, and mutated  
CC human spactin (autosomal recessive spastic ataxia of Charlevoix-Saguenay  
CC (ARSACS)) gene sequences (I). The spactin gene has been mapped to

CC chromosome 13q11. (I) have neuroprotective activities and can be used in  
CC gene therapy and as a spastin polypeptide agonists. (I), their fragments  
CC or their complements can be useful for assaying the presence of a nucleic  
CC acid molecule in a sample. (I) is useful for diagnosing or aiding in the  
CC diagnosis of an early onset neurodegenerative disease in an individual.  
CC The neurodegenerative disease comprises reduced sensory nerve conduction,  
CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres,  
CC atrophy of upper cerebellar vermis, absence of Purkinje cells and  
CC abnormal neuronal lipid storage. (I) can also be used to produce  
CC antisense nucleic acids, is useful as molecular weight or chromosome  
CC markers, to identify genetic disorders, as hybridisation probes or  
CC primers, as an antigen, identify and express recombinant protein for  
CC analysis, characterisation or therapeutic use, or as markers for tissues  
CC in which the corresponding protein is expressed. Diagnostic methods from  
CC the present invention can be used to identify subjects having or at risk  
CC of developing a disease or disorder associated with aberrant expression  
CC or activity of (I). The assays can be utilised to identify a subject  
CC having or at risk of developing a disorder associated with Spastin  
CC protein or spastin gene expression or activity. AAB20122 to AAB20173  
CC represent specifically claimed primers which can be used in diagnostic  
CC methods from the present invention  
CC  
XX

SO Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 5; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.78;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGATGGCCACTTTGGACT 20  
1 GTGATGGCCACTTTGGACT 20  
Db 1 GTGATGGCCACTTTGGACT 20

RESULT 2  
AB141475  
ID AB141475 standard; DNA; 25 BP.  
XX  
AC AB141475;  
XX

DT 27-AUG-2002 (first entry)  
XX

DE Human DNA-PK interaction protein 75 RT-PCR primer, SEQ ID NO:3.  
XX

XX Human; DNA-PK interacting protein 75; KIP protein homologue;  
XX recombinant production; malignant tumour; cancer; blood disease;  
XX HIV infection; gene therapy; human immunodeficiency virus;  
XX developmental disorder; immune disorder; inflammatory condition;  
XX cystostatic; antiinflammatory; immunomodulator; reverse transcription-PCR;  
XX RT-PCR; primer; ss.  
XX

OS Homo sapiens.  
XX

XX CN1292385-A.  
XX

PD 25-APR-2001.  
XX

XX 10-OCT-1999; 99CN-00116950.  
XX

XX 10-OCT-1999; 99CN-00116950.  
XX

PR (SHAN-) SHANGHAI BODAO GENE TECHNOLOGY CO LTD.  
XX

PA Mao Y, Xie Y;  
XX

XX WPI; 2001-409811/44.  
XX

DR Polypeptide-human DNA-PK interaction protein 75 and polynucleotide coding  
PT this polypeptide.  
XX

XX Example 3; Page 13 (Disclosure); 25pp; Chinese.  
XX

CC The invention relates to human DNA-PK interaction protein 75 (AB08943)  
CC and nucleic acids encoding it (AB141474). The protein has a molecular

CC weight of 75 kD and has 34% identity and 62% homology over a 243 amino  
CC acid stretch with a Caenorhabditis elegans KIP protein homologue shown in  
CC Genbank accession number Z73098. The invention also relates to a method  
CC for the recombinant production of the protein, an antagonist of the  
CC protein, and the use of the protein, gene and antagonist in therapeutic  
CC applications. DNA-PK interaction protein 75 can be used in the treatment  
CC of a variety of diseases such as malignant tumours, blood diseases,  
CC developmental disorders, HIV (human immunodeficiency virus) infection,  
CC immune disorders and inflammatory conditions. Sequences AB141475-AB141476  
CC represent reverse transcription-PCR (RT-PCR) primers used in an  
CC exemplification of the invention to isolate human DNA-PK interaction  
CC protein 75 cDNA  
CC  
XX

SO Sequence 25 BP; 7 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 4; Length 25;  
Best Local Similarity 84.2%; Pred. No. 1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GTGATGGCCACTTTGGAC 19  
1 GTGATGGCCACTTTGGAC 19  
Db 1 GTGATGGCCACTTTGGAC 19

RESULT 3  
AB186991  
ID AB186991 standard; DNA; 24 BP.  
XX

AC AB186991;  
XX

DT 15-FEB-2002 (first entry)  
XX

DE Capture oligonucleotide Zip ID#2297 oligo #2.  
XX

XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;  
XX ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;  
XX infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;  
XX oncogene; tumour suppressor; human papillomavirus; forensic;  
XX environmental monitoring; food industry; feed industry; ss.  
XX

OS Synthetic.  
XX

XX W0200179548-A2.  
XX

XX 25-OCT-2001.  
XX

XX 04-APR-2001; 2001WO-US010958.  
XX

XX 14-APR-2000; 2000US-0197271P.  
XX

XX (CORR ) CORNELL RES FOUND INC.  
XX

XX Barany F, Zilvi M, Gerry NP, Favis R, Klaman R;  
XX

XX WPI; 2002-034366/04.  
XX

DR Designing capture oligonucleotide probes for use on a support to which  
XX complementary oligonucleotides hybridize with little mismatch.  
XX

PS Example 5; Fig 25; 300pp; English.  
XX

CC The present invention describes a method (M1) for designing capture  
CC oligonucleotide probes (I) for use on a support to which complementary  
CC oligonucleotide probes (II) will hybridise with little mismatch, where  
CC (I) have melting temperatures within a narrow range. The method is useful  
CC for detecting infectious diseases caused by bacterial infections, fungal  
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal  
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and  
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,  
CC Epstein-Barr virus and polio virus, and parasitic infectious agents  
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus  
CC medinis. The method is also useful for detecting genetic diseases such  
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.

CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes  
 CC involved in DNA amplification, replication, recombination or repair, the  
 CC cancer is specifically associated with a gene selected from BRCA1 gene,  
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The  
 CC method is also used for environmental monitoring, forensics and the food  
 CC and feed industry, detecting comprises scanning (using e.g. a scanning  
 CC electron microscope and infrared microscope) the support at the  
 CC particular sites and identifying if ligation of the oligonucleotide probe  
 CC sets occurred and correlating (using a computer) identified ligation to a  
 CC presence or absence of the target nucleotide sequences. AB182074 to  
 CC AB197546 represent oligonucleotide sequences used in the exemplification  
 CC of the present invention

XX Sequence 24 BP, 5 A, 5 C, 9 G, 5 T, 0 U, 0 Other;

Query Match 66.0%; Score 13.2; DB 6; Length 24;

Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGAATGCCACTTGCAC 19  
 DB 1 TGAAGGTCACCTTGCAC 18

#### RESULT 4

AB186990/C  
 ID AB186990 standard; DNA; 24 BP.

XX AB186990;

DT 15-FEB-2002 (first entry)

DE Capture oligonucleotide zip ID#2297 oligo #1.

XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;  
 KM ligation detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;  
 KM infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;  
 KM oncogene; tumour suppressor; human papillomavirus; forensic;  
 KM environmental monitoring; food industry; feed industry; ss.

OS Synthetic.

XX WO200179548-A2.

PD 25-OCT-2001.

PF 04-APR-2001; 2001WO-US010958.

PR 14-APR-2000; 2000US-0197271P.

XX (CORR ) CORNELL RES FOUND INC.

PA Barany F, Zilvi M, Gerry NP, Favis R, Kilman R;

PI WPI, 2002-034366/04.

PT Designing capture oligonucleotide probes for use on a support to which  
 PT complementary oligonucleotides hybridize with little mismatch.

XX Example 5; Fig 25; 300pp; English.

XX The present invention describes a method (M1) for designing capture  
 CC oligonucleotide probes (I1) for use on a support to which complementary  
 CC oligonucleotide probes (I2) will hybridize with little mismatch, where  
 CC (I1) have melting temperatures within a narrow range. The method is useful  
 CC for detecting infectious diseases caused by bacterial infectious agents  
 CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal  
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and  
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,  
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents  
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Diacunculus  
 CC medineisi. The method is also useful for detecting genetic diseases such  
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.

CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes  
 CC involved in DNA amplification, replication, recombination or repair, the  
 CC cancer is specifically associated with a gene selected from BRCA1 gene,  
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The  
 CC method is also used for environmental monitoring, forensics and the food  
 CC and feed industry, detecting comprises scanning (using e.g. a scanning  
 CC electron microscope and infrared microscope) the support at the  
 CC particular sites and identifying if ligation of the oligonucleotide probe  
 CC sets occurred and correlating (using a computer) identified ligation to a  
 CC presence or absence of the target nucleotide sequences. AB182074 to  
 CC AB197546 represent oligonucleotide sequences used in the exemplification  
 CC of the present invention

XX Sequence 24 BP, 5 A, 9 C, 5 G, 5 T, 0 U, 0 Other;

Query Match 66.0%; Score 13.2; DB 6; Length 24;

Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGAATGCCACTTGCAC 19  
 DB 24 TGAAGGTCACCTTGCAC 7

#### RESULT 5

AB259471  
 ID AB259471 standard; DNA; 20 BP.

XX AB259471;

DT 17-APR-2003 (first entry)

DE Human src-c chimERIC phosphothioate oligonucleotide SEQ ID NO:32.

XX Human; src-c; tyrosine kinase; src-c inhibitor; cytostatic; osteopathic;  
 KM antiinflammatory; antibacterial; antisense therapy; vaccine; cancer;  
 KM antisense oligonucleotide; aberrant bone remodeling; breast cancer;  
 KM hyperproliferative disorder; pancreatic cancer; lung cancer; tumour;  
 KM ovarian cancer; oesophageal cancer; neuroblastoma; retinoblastoma;  
 KM Kaposi's sarcoma; infection; inflammation; tumour formation;  
 KM phosphothioate; ss.

OS Homo sapiens.

PD Synthetic.

PF Key Location/Qualifiers

FT modified\_base 1..20

FT modified\_base 1..20

FT modified\_base 1..20

FT modified\_base 1..20

FT modified\_base 1..20

XX WO200295053-A2.

PD 28-NOV-2002.

PF 16-MAY-2002; 2002WO-US015684.

PR 18-MAY-2001; 2001US-00860473.

XX (ISIS-) ISIS PHARM INC.

PI Bennett FC, Watt AT;

XX WPI; 2003-120806/11.

PT New antisense oligonucleotides targeted to nucleic acids encoding src-c,  
PT useful for diagnosing, treating or preventing diseases associated with  
PT the expression of src-c, e.g. cancer or inflammation, and in research  
PT applications.

PS Claim 3; Page 90; 137pp; English.

XX The present invention describes a compound (I) that is 8-50 nucleobases  
CC in length targeted to a nucleic acid molecule encoding a 5'UTR, 3'UTR,  
CC coding region, intron region, exon region, stop codon, intron:exon  
CC junction, exon:exon junction, or 5' mRNA variant of src-c, and which  
CC specifically hybridizes with and inhibits the expression of src-c. (I)  
CC have cytoskeletal, antiinflammatory, osteopathic and antibacterial  
CC activities, and can be used in antisense therapy and in vaccines. The  
CC antisense compounds (I) can be used for modulating the expression of src-  
CC c and for treating diseases or conditions associated with expression of  
CC src-c, e.g. aberrant bone remodeling or hyperproliferative disorders,  
CC particularly cancer, such as breast cancer, pancreatic cancer, lung  
CC cancer, ovarian cancer, esophageal cancer, neuroblastoma, retinoblastoma  
CC or Kaposi's sarcoma. (I) are also useful for diagnostics, therapeutics,  
CC prophylaxis, e.g. to prevent or delay infection, inflammation or tumour  
CC formation, as research reagents and kits, and in distinguishing between  
CC functions of various members of a biological pathway. The present  
CC sequence represents a human src-c antisense chimeric phosphorothioate  
CC oligonucleotide, which is used in an example from the present invention  
XX  
SQ Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 65.0%; Score 13; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GGCCACTTTGCAC 19  
|||  
DB 4 GGCCACTTTGCAC 16

RESULT 6  
AAC90263  
ID AAC90263 standard; DNA; 21 BP.

AC AAC90263;

DT 14-MAR-2001 (first entry)

DE Primer SNORF33h 41F used to detect human SNORF33.

KM SNORF33; inflammation; arthritis; neurological disorder; infection;  
KW bone disease; respiratory disorder; asthma; cancer; cardiovascular; ss.

OS Homo sapiens.

PN WO200073449-A1.

PD 07-DEC-2000.

PF 26-MAY-2000; 2000WO-US014654.

PR 28-MAY-1999; 99US-00322257.

PR 06-OCT-1999; 99US-00413433.

PA (SYNA-) SYNAPTIC PHARM CORP.

PI Borowsky BE, Ogozalek KU, Jones KA;

DR WPI; 2001-025252/03.

XX Nucleic acid encoding a mammalian (human, rat and mouse) SNORF33 receptor  
PT which is useful for designing drugs for treating conditions such as a  
PT chronic and acute inflammation, arthritis, neurological disorders and  
PT microbial infections.

PS Disclosure; Page 123; 227pp; English.

XX The present invention relates to a mammalian SNORF33 receptor. SNORF33  
CC antagonists and agonists are used to treat abnormalities brought about by  
CC increased or decreased activity of the mammalian SNORF33 receptor. The  
CC receptor is useful as a tool for designing drugs for treating conditions  
CC such as chronic and acute inflammation, arthritis, neurological  
CC disorders, microbial infections, bone diseases, respiratory disorders  
CC such as asthma, cancers, cardiovascular disorders  
XX  
SQ Sequence 21 BP; 3 A; 6 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 4; Length 21;  
Best Local Similarity 87.5%; Pred. No. 5.4e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 ATGGCACTTTGCAC 20  
|||  
DB 2 ATGGCACTTTGCAC 17

RESULT 7  
ADD15186  
ID ADD15186 standard; DNA; 21 BP.

AC ADD15186;

DT 15-JAN-2004 (first entry)

DE Reverse PCR primer to amplify the human XIST gene.

KM human; ss; PCR; primer; XIST; mental disorder;

KW differential gene expression; psychosis; schizophrenia; mood disorder;  
KW bipolar; major depression; neuroleptic; antidepressant; gene therapy.

OS Homo sapiens.

PN WO2003039490-A2.

PD 15-MAY-2003.

PR 12-NOV-2002; 2002WO-US036663.

PR 09-NOV-2001; 2001US-0339252P.

PA (UYTE-) UNIV OFFICE TECHNOLOGY LICENSING STANFORD.

PI Akil H, Bunney WB, Burke S, Choudary PV, Cox DR, Evans S;

PI Jones BG, Li J, Lopez JF, Myers RM, Thompson R, Vawter MP,

PI Watson SJ;

DR WPI; 2003-441464/41.

XX Determining a predisposition to mental disorders utilizing differential  
PT gene expression, useful for diagnosing, and/or treating mood disorders or  
PT psychosis, including bipolar and major depression disorders and  
PT schizophrenia.

PS Example 1; Page 57; 85pp; English.

XX This invention relates to a novel method for determining a predisposition  
CC to mental disorders by utilizing differential gene expression.

CC Specifically, it refers to the differential gene expression of brain  
CC region specific nucleic acids that can be used to determine a prevalence  
CC of mental disorders with a gender bias. Accordingly, it comprises

CC contacting a patients biological sample with a reagent (e.g. antibody)  
CC that selectively associates with a polynucleotide given in the

CC specification, and detecting the level of reagent that associates to  
CC determine whether the subject has, or is predisposed for, a mental

CC disorder. As such, the present invention describes a method and  
CC compositions that are useful for diagnosing, and/or treating mental

CC disorders, such as psychosis e.g. schizophrenia or a mood disorder  
CC including bipolar and major depression disorders. These compositions have

CC neuroleptic and antidepressant activities and can be used to treat the

CC aforementioned conditions via gene therapy routes. This oligonucleotide  
CC sequence is a PCR primer used to amplify the differentially expressed  
CC human XIST gene of the invention.

XX Sequence 21 BP; 3 A; 6 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 9; Length 21;  
Best Local Similarity 87.5%; Pred. No. 5.4e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ATGGCCACTTTGCACT 20  
Db 2 ATGGCCACTGTGACT 17

RESULT 8  
ACH54316  
ID ACH54316 standard; DNA; 25 BP.

XX ACH54316;  
AC  
DT 16-OCT-2003 (first entry)

XX DNA target sequence #3452 useful in array for genetic analyses.

XX Gene expression analysis; array; hybridisation; genetic variation;  
XX tag-labelled compound; gene family; in situ hybridisation;  
XX library screening; Southern hybridisation; northern hybridisation;  
XX dot-blot hybridisation; gene sequence; mutation detection;  
XX target sequence; probe; PCR; primer; ss.

XX Unidentified.

XX US2003082596-A1.

XX 01-MAY-2003.

XX 08-AUG-2002; 2002US-00215112.

XX 08-AUG-2001; 2001US-0311040P.

XX (MITT/) MITTMANN M.

XX Miltmann M;

XX WPI; 2003-576608/54.

XX New probe array useful e.g. for monitoring gene expression levels, for  
XX analyzing genetic variations, or for hybridizing tag-labeled compounds,  
XX comprises multiple nucleic acid probes.

XX Claim 1; SEQ ID NO 3452; 9pp; English.

XX The present invention relates to nucleic acid sequences that are  
XX complementary to particular genes, and can be used as probes for a  
XX variety of analyses, such as gene expression analysis. Each probe  
XX comprises 9 or more consecutive nucleotides from at least one of 14936  
XX nucleotide sequences defined in the patent, or their perfect sense match,  
XX sense mismatch, antisense match or antisense mismatch oligonucleotides.

XX The probes may be used in an array comprising at least 10 distinct  
XX nucleic acid probes. The array is useful in monitoring gene expression  
XX levels by hybridisation to a DNA library, in analyzing genetic

XX variations, and in hybridizing tag-labeled compounds. The probes are  
XX useful for identifying family members of a gene. The probes are also

XX useful in situ hybridisations, in screening cDNA or genomic libraries  
XX (or derived subclones) for additional clones containing segments of DNA

XX that have been previously isolated and sequenced, in Southern, northern,  
XX or dot-blot hybridisation of genomic DNA to identify or detect the

XX sequence of any gene or detect specific mutations in any gene, and in  
XX mapping the 5' terminus of mRNA molecules by primer extensions. The

XX nucleic acid sequences of the invention are also useful as PCR primers.  
XX The invention provides a large collection of nucleic acid sequences

XX complementary to particular genes with a wide range of analytical uses.

CC ACH50865-ACH65260 represent the target sequences of the invention. Note:  
CC The sequence data for this patent was obtained in electronic format  
CC directly from the USPTO web site at [seqdata.uspto.gov/psipdsidentry.html](http://seqdata.uspto.gov/psipdsidentry.html)

XX Sequence 25 BP; 4 A; 5 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 8; Length 25;  
Best Local Similarity 87.5%; Pred. No. 5.6e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAATGGCCACTTTGC 17  
Db 1 TGAATGGCCACTTTTC 16

RESULT 9  
ABV84997/C  
ID ABV84997 standard; DNA; 21 BP.

XX ABV84997;  
AC  
DT 12-DEC-2002 (first entry)

XX Human glypican 3 sense RT-PCR primer, SEQ ID NO:807.

XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;  
XX CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;  
XX expression pattern; differential expression; reverse transcription-PCR;  
XX RT-PCR; primer; ss.

XX Homo sapiens.

XX JP2002209591-A.

XX 30-JUL-2002.

XX 19-JAN-2001; 2001JP-00012328.

XX 19-JAN-2001; 2001JP-00012328.

XX (KAGA-) KAGAKU GIYUTSU SHINKO JIGYODAN.

XX WPI; 2002-631294/68.

XX Human chronic hepatitis C tissue expression exasperating gene group  
XX comprises 100 high-ranking genes.

XX Disclosure; Page 130; 139pp; Japanese.

XX The invention relates to SAGE (serial analysis of gene expression) tags  
XX representing groups of genes which are differentially expressed in human  
XX chronic hepatitis C (CH) liver tissue or hepatitis C-induced

XX hepatocellular carcinoma (HCC) compared with normal human liver tissue.

XX The SAGE tags of this invention consist of a sequence of 10 nucleotides  
XX located downstream of the 5'-CATG-3' sequence motif lying nearest to the

XX polyA region of cDNAs derived from a variety of genes. These tags serve  
XX to uniquely identify each transcript and can thus be used to analyse the

XX pattern of gene expression in particular cell types. The invention also  
XX relates to proteins encoded by the genes expressed in chronic hepatitis C

XX liver tissue or HCC, antibodies against these proteins, and inhibitors of  
XX the expression of groups of genes that are overexpressed in chronic

XX hepatitis C liver tissue or HCC. Groups of genes differentially expressed  
XX in chronic hepatitis C tissue or HCC may be used for the diagnosis and

XX treatment of these diseases. Such genes, inhibitors of their expression  
XX or activity, and antibodies against the gene products may be used in the

XX development of drugs to treat chronic hepatitis C and/or HCC. Sequences  
XX ABV84991-ABV85010 represent reverse transcription-PCR primers used in the

XX SAGE protocol to determine gene expression patterns in chronic hepatitis  
XX C liver tissue and hepatocellular carcinoma compared with normal liver  
XX tissue

XX Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 63.0%; Score 12.6; DB 6; Length 21;  
Best Local Similarity 78.9%; Pred. No. 7e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

2 TGAATGGCCACTTTGGACT 20  
19 TGCATGACCACTTGCAGT 1

Db

RESULT 10  
ACI25331/c  
ID ACI25331 standard; DNA; 25 BP.  
XX  
AC ACI25331;  
XX  
DT 13-OCT-2003 (first entry)  
XX  
DE Human microarray DNA oligonucleotide SEQ ID NO 25322.  
XX  
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; diallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX  
OS Homo sapiens.  
XX  
PN US2003104410-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 15-MAR-2002; 2002US-00098263.  
XX  
PR 16-MAR-2001; 2001US-0276759P.  
XX  
PA (AFFY-) AFFYMETRIX INC.  
XX  
PI Miltmann MP;  
XX  
DR WPI; 2003-567953/53.  
XX  
PT New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 25322; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic  
XX acid probes including one of 2,018,500 fully defined sequences, or its  
XX perfect match, perfect mismatch, antisense match or antisense mismatch.  
XX Also disclosed is a method of gene expression analysis. The array is used  
XX in monitoring gene expression levels by hybridisation to a DNA library,  
XX in analysis of genetic variation or in hybridisation of tag-labelled  
XX compounds. The nucleic acid probes are specifically designed for analysis  
XX of at least one target sequence. The method of analysis comprises  
XX hybridising at least one or more nucleic acids to at least two or more  
XX nucleic acid probes and detecting the hybridisation. The nucleic acid  
XX probes are attached to a solid support. The analysis comprises monitoring  
XX gene expression levels, identifying diallelic markers or polymorphisms,  
XX or family members of a gene and a cross-species comparison. Each of the  
XX nucleic acids further comprises a tag sequence. The array of nucleic acid  
XX probes is useful in situ hybridisation, in Southern, Northern or dot-  
XX blot hybridisation to identify or detect the sequence or specific  
XX mutations of any gene, in mapping the 5' termini of mRNA molecules by  
XX primer extensions or in screening cDNA or genomic libraries or subclones  
XX for additional subclones containing segments of DNA that have been  
XX isolated and previously sequenced. The sequence presented is one of the  
XX nucleic acid probes incorporated in the microarray. Note: The sequence  
XX data for this patent can also be obtained in electronic format directly  
XX from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

Seq Sequence 25 BP; 8 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 63.0%; Score 12.6; DB 8; Length 25;  
Best Local Similarity 78.9%; Pred. No. 7.2e+03;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 GTGAATGGCCACTTTGCAC 19  
19 GTTAACTTCACCTTGCAC 1

Db

RESULT 11  
ACI94288/c  
ID ACI94288 standard; DNA; 25 BP.  
XX  
AC ACI94288;  
XX  
DT 14-OCT-2003 (first entry)  
XX  
DE Human microarray DNA oligonucleotide SEQ ID NO 94279.  
XX  
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; diallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX  
OS Homo sapiens.  
XX  
PN US2003104410-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 15-MAR-2002; 2002US-00098263.  
XX  
PR 16-MAR-2001; 2001US-0276759P.  
XX  
PA (AFFY-) AFFYMETRIX INC.  
XX  
PI Miltmann MP;  
XX  
DR WPI; 2003-567953/53.  
XX  
PT New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 94279; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic  
XX acid probes including one of 2,018,500 fully defined sequences, or its  
XX perfect match, perfect mismatch, antisense match or antisense mismatch.  
XX Also disclosed is a method of gene expression analysis. The array is used  
XX in monitoring gene expression levels by hybridisation to a DNA library,  
XX in analysis of genetic variation or in hybridisation of tag-labelled  
XX compounds. The nucleic acid probes are specifically designed for analysis  
XX of at least one target sequence. The method of analysis comprises  
XX hybridising at least one or more nucleic acids to at least two or more  
XX nucleic acid probes and detecting the hybridisation. The nucleic acid  
XX probes are attached to a solid support. The analysis comprises monitoring  
XX gene expression levels, identifying diallelic markers or polymorphisms,  
XX or family members of a gene and a cross-species comparison. Each of the  
XX nucleic acids further comprises a tag sequence. The array of nucleic acid  
XX probes is useful in situ hybridisation, in Southern, Northern or dot-  
XX blot hybridisation to identify or detect the sequence or specific  
XX mutations of any gene, in mapping the 5' termini of mRNA molecules by  
XX primer extensions or in screening cDNA or genomic libraries or subclones  
XX for additional subclones containing segments of DNA that have been  
XX isolated and previously sequenced. The sequence presented is one of the  
XX nucleic acid probes incorporated in the microarray. Note: The sequence  
XX data for this patent can also be obtained in electronic format directly  
XX from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

Seq Sequence 25 BP; 9 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 63.0%; Score 12.6; DB 8; Length 25;  
Best Local Similarity 78.9%; Pred. No. 7.2e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGAATGCGCACTTGGCACT 20  
 |||||  
 DB 25 TGAACGAGCACTTCCACT 7

## RESULT 12

AAQ70717/c  
 ID AAQ70717 standard; DNA; 20 BP.

AC AAQ70717;

XX 25-MAR-2003 (revised)

DT 22-FEB-1995 (first entry)

XX C-myc gene antisense oligo.

XX C-myc; oncogene; smooth muscle; antisense; phosphorothioate;  
 KW oligonucleotide; restenosis; ss.

XX Synthetic.

XX WO9415646-A1.

XX 21-JUL-1994.

XX 07-JAN-1994; 94WO-US0000265.

XX 07-JAN-1993; 93US-00004799.

XX (UVE-) UNIV JEFFERSON THOMAS.

XX Zaleski A, Shi Y;

XX WPI; 1994-248909/30.

XX Use of antisense oligonucleotides specific for c-myc - for modulating the  
 PT proliferation of smooth muscle cells, partic. for treating or preventing the  
 PT restenosis.

XX Example 12; Page 29; 52pp; English.

XX An oligonucleotide (AAQ70710) antisense to a segment of human c-myc mRNA  
 CC beginning with a translational initiation codon reduced neointima  
 CC formation in the coronary vasculature in a pig restenosis model. Activity  
 CC was compared to that of antisense oligos (AAQ70715-21) that targeted  
 CC other regions of c-myc mRNA. The oligo given in AAQ70717 targeted  
 CC nucleotides 365-384 of the 5' non-coding region and provided a lower  
 CC degree of growth inhibition than the AAQ70710 oligo. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)

XX Sequence 20 BP; 4 A; 9 C; 5 G; 2 T; 0 U; 0 Other;

XX Query Match 62.0%; Score 12.4; DB 2; Length 20;

XX Best Local Similarity 92.9%; Pred. No. 8.8e+03;

XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGCCACTTTGGCACT 20  
 |||||  
 DB 16 GGCGACTTTGGCACT 3

## RESULT 13

AA795341/c

ID AA795341 standard; DNA; 20 BP.

XX AA795341;

XX 20-APR-1998 (first entry)

XX Treatment of human melanoma using c-myc oligonucleotide 8.

XX Melanoma; c-myc oligonucleotide; c-myc mRNA; cis-platin; inhibition;  
 KW metastasis; treatment; proliferation; human; tumour; ss.

XX Synthetic.  
 OS Homo sapiens.

XX WO9736005-A1.

XX 02-OCT-1997.

XX 24-MAR-1997; 97WO-US004703.

XX 26-MAR-1996; 96US-0014089P.

XX (LYNX-) LYNX THERAPEUTICS INC.

XX Zuppi G;

XX WPI; 1997-489662/45.

XX Inhibiting proliferation of human melanoma cells with anti-c-myc  
 PT oligonucleotide(s) - particularly used together with cis-platin,  
 PT inhibits metastasis, induces regression or prevents further growth.

XX Claim 1; Page 22; 68pp; English.

XX This c-myc oligonucleotide is complementary to a sequence of human c-myc  
 CC mRNA and is used for inhibiting the proliferation of human melanoma cells  
 CC (HMC). The c-myc oligonucleotide is at least 10 bases long and inhibits  
 CC proliferation of HMC by at least 10 percent at 10 mu M, when the cells  
 CC are cultured at 37 degree. C in presence of serum. The method is  
 CC particularly used to treat human melanoma, and inhibits metastasis,  
 CC promotes regression or prevents any increase in tumour mass. The c-myc  
 CC oligonucleotide can be used together with cis-platin and which then  
 CC reduces resistance of tumour cells to cis-platin. The oncogene c-myc is  
 CC found to be essential for growth and metastasis of melanoma, and the c-  
 CC myc oligonucleotides are designed to target double-stranded DNA or single  
 CC stranded RNA. A combination of c-myc oligonucleotide and cis-platin is  
 CC more effective than either component used alone

XX Sequence 20 BP; 4 A; 9 C; 5 G; 2 T; 0 U; 0 Other;

XX Query Match 62.0%; Score 12.4; DB 2; Length 20;

XX Best Local Similarity 92.9%; Pred. No. 8.8e+03;

XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGCCACTTTGGCACT 20  
 |||||  
 DB 16 GGCGACTTTGGCACT 3

## RESULT 14

AA792550

ID AA792550 standard; DNA; 20 BP.

XX AA792550;

XX 13-SEP-1999 (first entry)

XX PCR primer used to amplify an ORF of Chlamydia pneumoniae.

XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;  
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;  
 KW neutralising epitope; PCR primer; ss.

XX Synthetic.

XX Chlamydia pneumoniae.

XX WO9927105-A2.

XX 03-JUN-1999.

XX 20-NOV-1998; 98WO-IB001890.

XX 21-NOV-1997; 97FR-00014673.



PR 04-NOV-1998; 98US-0107078P.  
 XX (GEST ) GENSET.  
 PA Griffais R;  
 PI WPI; 1993-357842/30.  
 DR Genome sequence of Chlamydia pneumoniae.  
 XX  
 PS Page 1520; Disclosure; 1912pp; English.  
 CC AAX91991-X97517 represent PCR primers used to amplify open reading frames  
 CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae  
 CC (see AAX91990). C. pneumoniae causes respiratory disease such as  
 CC pneumonia and bronchitis and is thought to be a contributing factor in  
 CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema  
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading  
 CC frames of the C. pneumoniae genome (see AAY34584-AAY3879) can be used  
 CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae  
 CC nucleotide sequences can also be used as immunogenic compositions,  
 CC especially where the vector directs the expression of a neutralising  
 CC epitope of C. pneumoniae  
 XX  
 SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 2; Length 20;  
 Best Local Similarity 92.9%; Pred. No. 8.8e+03;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGGCAGTTGGCACT 20  
 |||||  
 Db 2 GGGCAGTTGGCCT 15

RESULT 15  
 ID AAS62210/C  
 AC AAS62210; standard; DNA; 23 BP.  
 XX  
 AC AAS62210;  
 XX  
 DT 29-JAN-2002 (first entry)  
 XX  
 DE Porcine forward PCR primer for GAPDH.  
 XX  
 KM Pig; muscular steatosis-modulating factor; ss; metabolic; muscular; MSWF;  
 KM food supplement; obesity; hyperlipidaemia; atherosclerosis;  
 KM wound healing; tumour; amyotrophic lateral sclerosis; ALS; PCR primer.  
 XX  
 OS Sus scrofa.  
 XX  
 PN WO200179287-A2.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 12-APR-2001; 2001WO-CA000509.  
 XX  
 PR 17-APR-2000; 2000US-0197936P.  
 XX  
 PA (MIG ) CANADA AGRIC & AGRI-FOOD CANADA.  
 XX  
 PI Palin M, Pomar C, Garlepy C;  
 XX  
 DR WPI; 2002-017600/02.  
 XX

PT Prognosis and diagnosis of muscular steatosis, useful e.g. for selecting  
 PT animals for breeding, by measuring levels of specific markers, also  
 PT treating or inducing steatosis.  
 XX  
 PS Example 1; Page 41; 190pp; English.  
 XX  
 CC The invention relates to prognosis or diagnosis of muscular steatosis by  
 CC measuring the level of a muscular steatosis modulating factor (MSWF) in a

CC human or animal and comparing this with the level in a healthy control.  
 CC Any difference indicates presence of, or predisposition to, muscular  
 CC steatosis. The method is particularly used for diagnosis or prognosis of  
 CC muscular steatosis in mammals and birds, e.g. to select individuals as  
 CC founders in animal breeding. Also (ant)agonists of MSWF can be used to  
 CC treat, or induce (for increasing the fat content of food) muscular  
 CC steatosis, in humans and animals. The MSWF markers are also useful in the  
 CC study of diseases and conditions such as obesity, hyperlipidaemia,  
 CC atherosclerosis, wound healing, tumours and amyotrophic lateral sclerosis  
 CC (ALS). The present sequence is a PCR primer used to amplify a MSWF of the  
 CC invention from its gene  
 XX

SQ Sequence 23 BP; 5 A; 6 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 6; Length 23;  
 Best Local Similarity 92.9%; Pred. No. 9e+03;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 AATGGCAGCTTGGC 17  
 |||||  
 Db 17 AATGTCAGCTTGGC 4

Search completed: May 27, 2004, 01:16:28  
 Job time : 335 secs

Thu May 27 10:14:59 2004

us-09-693-205a-47.may20.rn1

Page 1

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 00:50:52 ; Search time 80 Seconds  
(without alignments)  
138.738 Million cell updates/sec

Title: US-09-693-205A-47

Perfect score: 20  
Sequence: 1 ggcacgttgac 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 519696

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/2/ina/5A-COMB.seq: \*  
2: /cgn2\_6/ptodata/2/ina/5B-COMB.seq: \*  
3: /cgn2\_6/ptodata/2/ina/6A-COMB.seq: \*  
4: /cgn2\_6/ptodata/2/ina/6B-COMB.seq: \*  
5: /cgn2\_6/ptodata/2/ina/PTUS-COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	65.0	20	4	US-09-860-473-92
2	12.4	62.0	20	3	US-08-827-036A-8
3	12.4	62.0	20	3	US-08-481-341-8
4	12.4	62.0	20	4	US-09-198-452A-1851
5	12.4	62.0	20	5	PCT-US94-00265-8
6	12.2	61.0	17	3	US-09-411-578-15
7	12.2	61.0	17	3	US-09-411-578-17
8	12.2	61.0	17	4	US-09-749-233-15
9	12.2	61.0	17	4	US-09-749-233-17
10	12.2	61.0	17	4	US-09-540-014-14
11	12	60.0	23	4	US-08-540-259-1
12	11.8	59.0	21	4	US-09-442-143A-29
13	11.4	57.0	20	3	US-09-323-743-54
14	11.4	57.0	20	3	US-09-323-743-55
15	11.4	57.0	20	3	US-09-323-743-56
16	11.4	57.0	20	3	US-09-323-743-57
17	11.4	57.0	21	2	US-08-665-202-129
18	11.4	57.0	21	2	US-08-847-844A-115
19	11.4	57.0	21	4	US-09-315-574-129
20	11.4	57.0	21	4	US-09-642-894A-7
21	11.4	57.0	23	2	US-08-359-705B-16
22	11.4	57.0	23	2	US-08-286-846A-16
23	11.4	57.0	23	2	US-08-457-880A-16
24	11.4	57.0	23	3	US-08-444-622A-16
25	11.4	57.0	23	3	US-08-943-552-16
26	11.4	57.0	23	3	US-09-156-923-16
27	11.4	57.0	24	4	US-08-759-436-10

28	11.2	56.0	18	3	US-09-205-143-68	Sequence 68, Appl
29	11.2	56.0	18	3	US-09-632-580A-20	Sequence 20, Appl
30	11.2	56.0	19	4	US-09-422-978-10969	Sequence 10969, A
31	11.2	56.0	20	3	US-09-487-445-82	Sequence 82, Appl
32	11.2	56.0	20	4	US-09-091-952A-98	Sequence 98, Appl
33	11.2	56.0	20	4	US-09-375-318-20	Sequence 20, Appl
34	11.2	56.0	21	1	US-08-308-949A-16	Sequence 16, Appl
35	11.2	56.0	21	4	US-09-079-812E-11	Sequence 11, Appl
36	11.2	56.0	22	4	US-09-823-545-28	Sequence 28, Appl
37	11.2	56.0	23	3	US-09-026-958-7	Sequence 7, Appl
38	11.2	56.0	23	4	US-09-612-033B-2	Sequence 35, Appl
39	11.2	56.0	23	4	US-09-798-051-12	Sequence 12, Appl
40	11.2	56.0	25	3	US-09-176-666-29	Sequence 29, Appl
41	11.2	56.0	20	3	US-08-894-816B-40	Sequence 40, Appl
42	11	55.0	20	3	US-08-894-816B-41	Sequence 41, Appl
43	11	55.0	20	4	US-09-445-472-20	Sequence 20, Appl
44	11	55.0	20	4	US-09-445-472-21	Sequence 21, Appl
45	11	55.0	20	4	US-09-445-472-21	Sequence 21, Appl

#### ALIGNMENTS

RESULT 1  
US-09-860-473-92  
Sequence 92, Application US/09860473  
Patent No. 6656732  
GENERAL INFORMATION:  
APPLICANT: Andrew T. Matt  
TITLE OF INVENTION: ANTISENSE MODULATION OF SRC-C EXPRESSION  
FILE REFERENCE: RUS-0222  
CURRENT APPLICATION NUMBER: US/09/860,473  
CURRENT FILING DATE: 2001-05-18  
NUMBER OF SEQ ID NOS: 169  
SEQ ID NO 92  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-860-473-92

Query Match 65.0%; Score 13; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 0;

QY 7 GGCACCTTGCAC 19  
|||||  
DB 4 GGCACCTTGCAC 16

RESULT 2  
US-08-827-036A-8/c  
Sequence 8, Application US/08827036A  
Patent No. 6080727  
GENERAL INFORMATION:  
APPLICANT: Gabriella Zupi  
TITLE OF INVENTION: Oligonucleotide Treatments and  
TITLE OF INVENTION: Compositions for Human Melanoma  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James A. Bradburne, Ph.D.  
STREET: 5 Palo Alto Square,  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94306-2155  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 3.1/DOS 5.0

```

SOFTWARE: Microsoft Word for Windows, vers. 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,036A
FILING DATE: 03/25/97
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 60/014,089
FILING DATE: 26-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: James A. Bradbire, Ph.D.
REGISTRATION NUMBER: 38,389
REFERENCE/DOCKET NUMBER: LYNX-031/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 843-5035
TELEFAX: (650) 857-0663
INFORMATION FOR SEQ. ID NO.: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-827-036A-8

Query Match      62.0%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 8.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      7 GGCCACTTGCCT 20
Db      16 GGGCACCTTGCACT 3

RESULT 3
US-08-481-341-8/c
Sequence 8, Application US/08481341
Patent No. 6159946
GENERAL INFORMATION:
APPLICANT: Zalewski, Andrew and Shi, Yi
TITLE OF INVENTION: ANTISENSE INHIBITION OF
TITLE OF INVENTION: C-MYC TO MODULATE THE PROLIFERATION
TITLE OF INVENTION: OF SMOOTH MUSCLE CELLS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Iavorogna
ADDRESSEE: & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS/DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,341
FILING DATE: January 7, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,799
FILING DATE: January 7, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Daniel A. Monaco
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-9 C11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ. ID NO.: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid

```

```

STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-481-341-8

Query Match          62.0%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 8.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      7 GGCCACTTGCACCT 20
      |||||
Db      16 GGCCACTTGCACCT 3

RESULT 4
US-09-198-452A-1851
Sequence 1851, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragm
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, p
FILE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198.452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1851
LENGTH: 20
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1851

Query Match          62.0%; Score 12.4; DB 4; Length 20;
Best Local Similarity 92.9%; Pred. No. 8.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      7 GGCCACTTGCACCT 20
      |||||
Db      2 GGCCACTTGCACCT 15

RESULT 5
PCT-US94-00265-8/C
Sequence 8, Application PC/TUS9400265
GENERAL INFORMATION:
APPLICANT: Thomas Jefferson University
TITLE OF INVENTION: ANTISENSE INHIBITION OF
TITLE OF INVENTION: C-MYC TO MODULATE THE PROLIFERATION
TITLE OF INVENTION: OF SMOOTH MUSCLE CELLS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Seidel, Gonda, Lavorigna
ADDRESSER: 6 Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS/DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00265
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 004.799
FILING DATE: January 7, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Daniel A. Monaco

```

Thu May 27 10:14:59 2004

us-09-693-205a-47.may20.rn1

Page 3

REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 8321-9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
ANTI-SENSE: yes  
PCT-US94-00265-8

Query Match 62.0%; Score 12.4; DB 5; Length 20;  
Best Local Similarity 92.9%; Pred. No. 8.2e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGCCACTTTGCACT 20  
DB 16 GGCCACTTTGCACT 3

RESULT 6  
US-09-411-578-15  
Sequence 15, Application US/09411578  
Patent No. 6203801  
GENERAL INFORMATION:  
APPLICANT: Schaad, Theodorus C  
APPLICANT: Kuiper, Catharina M  
APPLICANT: Vermeulen, Arnoldus N  
TITLE OF INVENTION: Coccioidosis Vaccines  
FILE REFERENCE: schaad  
CURRENT APPLICATION NUMBER: US/09/411,578  
CURRENT FILING DATE: 1999-10-04  
EARLIER APPLICATION NUMBER: 98203384.7  
EARLIER FILING DATE: 1998-10-07  
EARLIER APPLICATION NUMBER: 98203457.1  
EARLIER FILING DATE: 1998-10-16  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 15  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Eimeria tenella  
US-09-411-578-15

Query Match 61.0%; Score 12.2; DB 3; Length 17;  
Best Local Similarity 82.4%; Pred. No. 1e+03; 3; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGGCCACTTTGC 17  
DB 1 GTGAATGGCCACTTTGC 17

RESULT 7  
US-09-411-578-17  
Sequence 17, Application US/09411578  
Patent No. 6203801  
GENERAL INFORMATION:  
APPLICANT: Schaad, Theodorus C  
APPLICANT: Kuiper, Catharina M  
APPLICANT: Vermeulen, Arnoldus N  
TITLE OF INVENTION: Coccioidosis Vaccines  
FILE REFERENCE: schaad  
CURRENT APPLICATION NUMBER: US/09/411,578  
CURRENT FILING DATE: 1999-10-04  
EARLIER APPLICATION NUMBER: 98203384.7  
EARLIER FILING DATE: 1998-10-07  
EARLIER APPLICATION NUMBER: 98203457.1  
EARLIER FILING DATE: 1998-10-16  
NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 17  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Eimeria tenella  
US-09-411-578-17

Query Match 61.0%; Score 12.2; DB 3; Length 17;  
Best Local Similarity 82.4%; Pred. No. 1e+03; 3; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGGCCACTTTGC 17  
DB 1 GTGAATGGCCACTTTGC 17

RESULT 8  
US-09-749-233-15  
Sequence 15, Application US/09749233  
Patent No. 668061  
GENERAL INFORMATION:  
APPLICANT: Schaad, Theodorus C  
APPLICANT: Kuiper, Catharina M  
APPLICANT: Vermeulen, Arnoldus N  
TITLE OF INVENTION: Coccioidosis Vaccines  
FILE REFERENCE: schaad  
CURRENT APPLICATION NUMBER: US/09/749,233  
CURRENT FILING DATE: 2000-12-27  
PRIOR APPLICATION NUMBER: 09/411,578  
PRIOR FILING DATE: 1999-10-04  
PRIOR APPLICATION NUMBER: 98203457.1  
PRIOR FILING DATE: 1998-10-16  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 15  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Eimeria tenella  
US-09-749-233-15

Query Match 61.0%; Score 12.2; DB 4; Length 17;  
Best Local Similarity 82.4%; Pred. No. 1e+03; 3; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGGCCACTTTGC 17  
DB 1 GTGAATGGCCACTTTGC 17

RESULT 9  
US-09-749-233-17  
Sequence 17, Application US/09749233  
Patent No. 668061  
GENERAL INFORMATION:  
APPLICANT: Schaad, Theodorus C  
APPLICANT: Kuiper, Catharina M  
APPLICANT: Vermeulen, Arnoldus N  
TITLE OF INVENTION: Coccioidosis Vaccines  
FILE REFERENCE: schaad  
CURRENT APPLICATION NUMBER: US/09/749,233  
CURRENT FILING DATE: 2000-12-27  
PRIOR APPLICATION NUMBER: 09/411,578  
PRIOR FILING DATE: 1999-10-04  
PRIOR APPLICATION NUMBER: 98203457.1  
PRIOR FILING DATE: 1998-10-16  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 17  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Eimeria tenella  
US-09-749-233-17

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Query Match 61.0%; Score 12.2; DB 4; Length 17;  
Best Local Similarity 82.4%; Pred. No. 1e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGATGGCCACTTGC 17  
Db 1 GTGATGGCCACTTGC 17

RESULT 10  
US-09-540-014-14/c  
Sequence 14, Application US/09540014  
Patent No. 6380372  
GENERAL INFORMATION:  
APPLICANT: Cho, Myeong-Je  
APPLICANT: Del Val, Greg  
APPLICANT: Gallau, Maxime  
APPLICANT: Lemaux, Peggy G.  
APPLICANT: Buchanan, Bob B.  
TITLE OF INVENTION: Barley Gene for Thiodoxin and  
TITLE OF INVENTION: NADP-Thiodoxin Reductase  
FILE REFERENCE: 2001-0701.30  
CURRENT APPLICATION NUMBER: US/09/540,014  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: US 60/127,198  
PRIOR FILING DATE: 1999-03-31  
PRIOR APPLICATION NUMBER: US 60/169,162  
PRIOR FILING DATE: 1999-12-06  
PRIOR APPLICATION NUMBER: US 60/177,740  
PRIOR FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: US 60/177,739  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: degenerative primer  
US-09-540-014-14

Query Match 61.0%; Score 12.2; DB 4; Length 23;  
Best Local Similarity 57.9%; Pred. No. 1.1e+03;  
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGATGGCCACTTGCAC 19  
Db 21 GTGATGGCCACTTGCAC 3

RESULT 11  
US-08-540-259-1  
Sequence 1, Application US/08540259  
Patent No. 6013516  
GENERAL INFORMATION:  
APPLICANT: Verma, Indar  
APPLICANT: Trono, Didier  
APPLICANT: Naldini, Luigi  
APPLICANT: Galley, Philippe  
TITLE OF INVENTION: VECTOR AND METHOD OF USE FOR NUCLEIC  
TITLE OF INVENTION: ACID DELIVERY TO NON-DIVIDING CELLS  
FILE REFERENCE: 07251/002001  
CURRENT APPLICATION NUMBER: US/08/540,259  
CURRENT FILING DATE: 1995-10-06  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: oligonucleotide for PCR

US-08-540-259-1  
Query Match 60.0%; Score 12; DB 3; Length 23;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTGATGGCCACTTGCAC 20  
Db 1 GTGATGGCCACTTGCAC 20

RESULT 12  
US-09-442-143A-29/c  
Sequence 29, Application US/09442143A  
Patent No. 6403089  
GENERAL INFORMATION:  
APPLICANT: Levy, Gary  
APPLICANT: Clark, David A.  
TITLE OF INVENTION: Methods of Modulating Immune Coagulation  
FILE REFERENCE: 9579-14  
CURRENT APPLICATION NUMBER: US/09/442,143A  
PRIOR FILING DATE: 1999-11-15  
PRIOR APPLICATION NUMBER: US 60/046,537  
PRIOR FILING DATE: 1997-05-17  
PRIOR APPLICATION NUMBER: US 60/061,684  
PRIOR FILING DATE: 1997-10-10  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn Version 3.1  
SEQ ID NO 29  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Primer  
US-09-442-143A-29

Query Match 59.0%; Score 11.8; DB 4; Length 21;  
Best Local Similarity 86.7%; Pred. No. 1.8e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAATGGCCACTTGC 17  
Db 19 GATTCGCCACTTGC 5

RESULT 13  
US-09-323-743-54/c  
Sequence 54, Application US/09323743  
Patent No. 6214986  
GENERAL INFORMATION:  
APPLICANT: Bennett, C. Frank  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Wonda, Brett P.  
APPLICANT: Nickoloff, Brian J.  
APPLICANT: Zhang, Qingsong  
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
FILE REFERENCE: ISPH-0368  
CURRENT APPLICATION NUMBER: US/09/323,743  
CURRENT FILING DATE: 1999-06-01  
EARLIER APPLICATION NUMBER: 09/277,020  
EARLIER FILING DATE: 1998-03-26  
EARLIER APPLICATION NUMBER: 09/167,921  
EARLIER FILING DATE: 1998-10-07  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 54  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-323-743-54

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Query Match 57.0%; Score 11.4; DB 3; Length 20;  
Best Local Similarity 92.3%; Pred. No. 2.9e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 2 TGAATGGCCACTT 14  
Db 13 TGGATGGCCACTT 1

RESULT 14  
US-09-323-743-55/C  
Sequence 55, Application US/09323743  
Patent No. 6214986  
GENERAL INFORMATION:  
APPLICANT: Bennett, C. Frank  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Monia, Brett P.  
APPLICANT: Nickoloff, Brian J.  
APPLICANT: Zhang, Qingqing  
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
FILE REFERENCE: ISPH-0368  
CURRENT APPLICATION NUMBER: US/09/323,743  
CURRENT FILING DATE: 1999-06-01  
EARLIER APPLICATION NUMBER: 09/277,020  
EARLIER FILING DATE: 1998-03-26  
EARLIER APPLICATION NUMBER: 09/167,921  
EARLIER FILING DATE: 1998-10-07  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 55  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-323-743-55

Query Match 57.0%; Score 11.4; DB 3; Length 20;  
Best Local Similarity 92.3%; Pred. No. 2.9e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 2 TGAATGGCCACTT 14  
Db 15 TGGATGGCCACTT 3

RESULT 15  
US-09-323-743-56/C  
Sequence 56, Application US/09323743  
Patent No. 6214986  
GENERAL INFORMATION:  
APPLICANT: Bennett, C. Frank  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Monia, Brett P.  
APPLICANT: Nickoloff, Brian J.  
APPLICANT: Zhang, Qingqing  
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
FILE REFERENCE: ISPH-0368  
CURRENT APPLICATION NUMBER: US/09/323,743  
CURRENT FILING DATE: 1999-06-01  
EARLIER APPLICATION NUMBER: 09/277,020  
EARLIER FILING DATE: 1998-03-26  
EARLIER APPLICATION NUMBER: 09/167,921  
EARLIER FILING DATE: 1998-10-07  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 56  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-323-743-56

Query Match 57.0%; Score 11.4; DB 3; Length 20;  
Best Local Similarity 92.3%; Pred. No. 2.9e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 2 TGAATGGCCACTT 14  
Db 17 TGGATGGCCACTT 5

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Job time : 81 secs

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CM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 01:42:23 ; Search time 312 Seconds  
(without alignments)  
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Title: US-09-693-205a-47

Perfect score: 20  
Sequence: 1 gtgaatggccacttgcact 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2953838 seqs, 2272363821 residues

Total number of hits satisfying chosen parameters: 1135042

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA:\*

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3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
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6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
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15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US10C\_NEW\_PUB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.2	66.0	20	17	US-10-210-479-73
2	13.2	66.0	20	17	US-10-210-479-119
3	12.8	64.0	21	15	US-10-267-217-82
4	12.8	64.0	21	15	US-10-283-582-33
5	12.8	64.0	23	15	US-10-215-112-3452
6	12.6	63.0	25	15	US-10-098-263B-25322
7	12.6	63.0	25	15	US-10-098-263B-94279
8	12.4	62.0	20	16	US-10-289-762-1851
9	12.4	62.0	24	10	US-09-940-185-1813
10	12.2	61.0	20	13	US-10-215-821-45
11	12.2	61.0	22	15	US-10-131-827-9031
12	12.2	60.0	23	15	US-10-093-841-64
13	12	60.0	23	10	US-09-892-949-6
14	12	60.0	25	13	US-10-358-228-12

C 15	12	60.0	25	15	US-10-098-263B-43779	Sequence 43779, A
C 16	11.8	59.0	20	16	US-10-190-366-23	Sequence 23, Appl
C 17	11.8	59.0	20	16	US-10-190-366-86	Sequence 86, Appl
C 18	11.8	59.0	20	16	US-10-190-366-220	Sequence 220, App
C 19	11.8	59.0	20	16	US-10-190-366-283	Sequence 283, App
C 20	11.8	59.0	20	17	US-10-211-908-74	Sequence 74, Appl
C 21	11.8	59.0	21	10	US-09-902-563-29	Sequence 29, Appl
C 22	11.8	59.0	21	15	US-10-096-255-29	Sequence 29, Appl
C 23	11.8	59.0	22	8	US-08-812-93A-42	Sequence 42, Appl
C 24	11.8	59.0	22	11	US-09-774-681-42	Sequence 42, Appl
C 25	11.8	59.0	22	13	US-10-262-511-119	Sequence 319, App
C 26	11.8	59.0	22	13	US-10-187-975-147	Sequence 147, App
C 27	11.8	59.0	25	15	US-10-215-112-8251	Sequence 8251, Ap
C 28	11.6	58.0	20	16	US-10-296-540-60	Sequence 60, Appl
C 29	11.6	58.0	21	13	US-10-431-599-14	Sequence 14, Appl
C 30	11.6	58.0	25	15	US-10-098-263B-56871	Sequence 56871, A
C 31	11.6	58.0	25	15	US-10-098-263B-76311	Sequence 76311, A
C 32	11.6	58.0	25	15	US-10-098-263B-76312	Sequence 76312, A
C 33	11.6	58.0	25	15	US-10-098-263B-80220	Sequence 80220, A
C 34	11.4	57.0	18	15	US-10-213-770A-14	Sequence 14, Appl
C 35	11.4	57.0	20	9	US-09-734-846-54	Sequence 54, Appl
C 36	11.4	57.0	20	9	US-09-734-846-55	Sequence 55, Appl
C 37	11.4	57.0	20	9	US-09-734-846-56	Sequence 56, Appl
C 38	11.4	57.0	20	9	US-09-734-846-57	Sequence 57, Appl
C 39	11.4	57.0	20	9	US-09-745-317-83	Sequence 83, Appl
C 40	11.4	57.0	20	9	US-09-745-317-87	Sequence 87, Appl
C 41	11.4	57.0	20	10	US-09-953-562-23	Sequence 23, Appl
C 42	11.4	57.0	20	15	US-10-302-262-54	Sequence 54, Appl
C 43	11.4	57.0	20	15	US-10-302-262-55	Sequence 55, Appl
C 44	11.4	57.0	20	15	US-10-302-262-56	Sequence 56, Appl
C 45	11.4	57.0	20	15	US-10-302-262-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1  
US-10-210-479-73  
; Sequence 73, Application US/10210479  
; Publication No. US20040023380A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR 6 EXPRESSIC  
; FILE REFERENCE: RTS-0385  
; CURRENT APPLICATION NUMBER: US/10/210,479  
; CURRENT FILING DATE: 2002-07-31  
; NUMBER OF SEQ ID NOS: 123  
; SEQ ID NO 73  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-210-479-73

Query Match 66.0% Score 13.2; DB 17; Length 20;  
Best Local Similarity 83.3% Pred. No. 5.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Db 3 GAATGCGCACTTGCACT 20  
1 GAAGGCGCACTTGCACT 18  
RESULT 2  
US-10-210-479-119/c  
; Sequence 119, Application US/10210479  
; Publication No. US20040023380A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Kenneth W. Doble  
; TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR 6 EXPRESSIC

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FILE REFERENCE: RTS-0385  
CURRENT APPLICATION NUMBER: US/10/210.479  
CURRENT FILING DATE: 2002-07-31  
NUMBER OF SEQ ID NOS: 123  
SEQ ID NO 119  
LENGTH: 20  
TYPE: DNA  
ORGANISM: H. sapiens  
FEATURE:  
US-10-210-479-119

Query Match 66.0%; Score 13.2; DB 17; Length 20;  
Best Local Similarity 83.3%; Pred. No. 5.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GAATGGCCACTTTGGCACT 20  
DB 20 GAATGGCCACTTTGGCACT 3

RESULT 3  
US-10-267-217-22  
Sequence 22, Application US/10267217  
Publication No. US20030105318A1  
GENERAL INFORMATION:  
APPLICANT: Borowsky, Beth E.  
APPLICANT: Ogozalek, Kristine L.  
APPLICANT: Jones, Kenneth A.  
TITLE OF INVENTION: DNA Encoding SNORF33 Receptor  
FILE REFERENCE: 59338A  
CURRENT APPLICATION NUMBER: US/10/267.217  
CURRENT FILING DATE: 2002-10-07  
PRIOR APPLICATION NUMBER: US/09/413.433  
PRIOR FILING DATE: 1999-10-06  
PRIOR APPLICATION NUMBER: 09/322.257  
PRIOR FILING DATE: 1999-05-28  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn Ver. 2.0 - Beta  
SEQ ID NO 22  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer/probe  
US-10-267-217-22

Query Match 64.0%; Score 12.8; DB 15; Length 21;  
Best Local Similarity 87.5%; Pred. No. 8.5e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ATGGCCACTTTGGCACT 20  
DB 2 ATGGCCACTTTGGCACT 17

RESULT 4  
US-10-293-582-33  
Sequence 33, Application US/10293582  
Publication No. US20030175253A1  
GENERAL INFORMATION:  
APPLICANT: Akil, Huda  
APPLICANT: Bunney, William E.  
APPLICANT: Burke, Sharon  
APPLICANT: Choudary, Prabhakara V.  
APPLICANT: Cox, David R.  
APPLICANT: Evans, Simon  
APPLICANT: Jones, Edward G.  
APPLICANT: Li, Jun  
APPLICANT: Lopez, Juan F.  
APPLICANT: The Trustees of The Ieland Stanford Junior University  
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating  
FILE REFERENCE: 020885-000210US

CURRENT APPLICATION NUMBER: US/10/293.582  
CURRENT FILING DATE: 2002-11-12  
PRIOR APPLICATION NUMBER: US 60/339,252  
PRIOR FILING DATE: 2001-11-09  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 33  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: reverse PCR  
US-10-293-582-33

Query Match 64.0%; Score 12.8; DB 15; Length 21;  
Best Local Similarity 87.5%; Pred. No. 8.5e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ATGGCCACTTTGGCACT 20  
DB 2 ATGGCCACTTTGGCACT 17

RESULT 5  
US-10-215-112-3452  
Sequence 3452, Application US/10215112  
Publication No. US20030082596A1  
GENERAL INFORMATION:  
APPLICANT: Michael, Miltman  
TITLE OF INVENTION: Method of Genetic Analysis of Probes:  
FILE REFERENCE: 3119  
CURRENT APPLICATION NUMBER: US/10/215.112  
CURRENT FILING DATE: 2002-08-08  
NUMBER OF SEQ ID NOS: 14936  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3452  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-215-112-3452

Query Match 64.0%; Score 12.8; DB 15; Length 25;  
Best Local Similarity 87.5%; Pred. No. 8.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGAATGGCCACTTTGC 17  
DB 1 TGAATGGCCACTTTTC 16

RESULT 6  
US-10-098-263B-25322/c  
Sequence 25322, Application US/10098263B  
Publication No. US20030104410A1  
GENERAL INFORMATION:  
APPLICANT: Miltman, Michael  
TITLE OF INVENTION: Human Microarray  
FILE REFERENCE: 3118.1  
CURRENT APPLICATION NUMBER: US/10/098.263B  
CURRENT FILING DATE: 2003-01-08  
PRIOR APPLICATION NUMBER: 60/276,759  
PRIOR FILING DATE: 2001-03-16  
NUMBER OF SEQ ID NOS: 131066  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 25322  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-098-263B-25322



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Query Match      63.0%; Score 12.6; DB 15; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GTGATGGCCACTTTGCAC 19
DB      19 GTTAACTCCACTTTGCAC 1

RESULT 7
US-10-098-263B-94279/c
; Sequence 94279, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mitteran, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 94279
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-94279

Query Match      63.0%; Score 12.6; DB 15; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TGAATGGCCACTTTGCAC 20
DB      25 TGAACAGGCACCTTCCACT 7

RESULT 8
US-10-289-762-1851
; Sequence 1851, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT FILING DATE: 2003-03-27
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1851
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-1851

Query Match      62.0%; Score 12.4; DB 16; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GGCCACTTTGCAC 20
DB      2 GGCCACTTTGCAC 15

RESULT 9
US-09-940-185-3813/c
; Sequence 3813, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin

Query Match      62.0%; Score 12.4; DB 10; Length 24;
Best Local Similarity 92.9%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 GAATGGCCACTTTG 16
DB      23 GAATGGCCACTTTG 10

RESULT 10
US-10-215-821-45
; Sequence 45, Application US/10215821
; Publication No. US20040029274A1
; GENERAL INFORMATION:
; APPLICANT: Jacquelline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF EDG5 EXPRESSION
; FILE REFERENCE: RNS-0155
; CURRENT FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 111
; SEQ ID NO 45
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-215-821-45

Query Match      61.0%; Score 12.2; DB 13; Length 20;
Best Local Similarity 92.4%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 AATGGCCACTTTGCAC 20
DB      3 AATGGCCACTTTGCAC 19

RESULT 11
US-10-131-827-9031/c
; Sequence 9031, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMM
; FILE REFERENCE: 506612000120
; CURRENT FILING DATE: 2002-09-06
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
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PRIOR FILING DATE: 2001-06-08  
NUMBER OF SEQ ID NOS: 9090  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 9031  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Primer  
US-10-131-827-9031

Query Match 61.0%; Score 12.2; DB 16; Length 22;  
Best Local Similarity 82.4%; Pred. No. 1.8e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGATGGCCACTTGGCA 18  
Db 17 TGATGGCCACTGCA 1

RESULT 12  
US-10-091-841-14/c  
Sequence 14, Application US/10091841  
Publication No. US20030150010A1  
GENERAL INFORMATION:  
APPLICANT: Cho, Myeong-Je  
APPLICANT: Del Val, Greg  
APPLICANT: Caillaud, Maxime  
APPLICANT: Lemauz, Peggy G.  
APPLICANT: Bucharan, Bob B.  
TITLE OF INVENTION: Barley Gene for Thioresdoxin and  
FILE REFERENCE: 2001-0701.30  
CURRENT FILING DATE: 2002-03-05  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 09/540,014  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: US 60/127,138  
PRIOR FILING DATE: 1999-03-31  
PRIOR APPLICATION NUMBER: US 60/169,162  
PRIOR FILING DATE: 1999-12-06  
PRIOR APPLICATION NUMBER: US 60/177,740  
PRIOR FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: US 60/177,739  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: degenerative primer  
US-10-091-841-14

Query Match 61.0%; Score 12.2; DB 15; Length 23;  
Best Local Similarity 57.9%; Pred. No. 1.8e+04;  
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGATGGCCACTTGGCA 19  
Db 21 GTGATGGCCACTTGGCA 3

RESULT 13  
US-09-892-949-6/c  
Sequence 6, Application US/09892949  
Publication No. US20030096339A1  
GENERAL INFORMATION:  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Presnell, Scott R.  
APPLICANT: Gao, Zeren  
APPLICANT: Whitmore, Theodore E.

APPLICANT: Kulper, Joseph L.  
APPLICANT: Maurer, Mark F.  
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17  
FILE REFERENCE: 00-42  
CURRENT APPLICATION NUMBER: US/09/892,949  
CURRENT FILING DATE: 2001-06-26  
PRIOR APPLICATION NUMBER: US 60/214,282  
PRIOR FILING DATE: 2000-06-26  
PRIOR APPLICATION NUMBER: US 60/214,955  
PRIOR FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: US 60/267,963  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide primer ZC27898  
US-09-892-949-6

Query Match 60.0%; Score 12; DB 10; Length 23;  
Best Local Similarity 75.0%; Pred. No. 2.2e+04;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GTGATGGCCACTTGGCACT 20  
Db 22 GTGATGGCCACTTGGCACT 3

RESULT 14  
US-10-358-228-12/c  
Sequence 12, Application US/10358228  
Publication No. US20030211578A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc. et al.  
TITLE OF INVENTION: Interferon Receptor HKAEF92  
FILE REFERENCE: PF465C1  
CURRENT APPLICATION NUMBER: US/10/358,228  
CURRENT FILING DATE: 2003-02-05  
PRIOR APPLICATION NUMBER: 09/453,569  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: 09/326,216  
PRIOR FILING DATE: 1999-06-03  
PRIOR APPLICATION NUMBER: 60/088,185  
PRIOR FILING DATE: 1998-06-05  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: Primer Bind  
OTHER INFORMATION: Synthetic primer complementary to the INFR-HKAEF92 protein;  
OTHER INFORMATION: Includes a NdeI restriction site.  
US-10-358-228-12

Query Match 60.0%; Score 12; DB 13; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.3e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GAATGGCCACTT 14  
Db 25 GAATGGCCACTT 14

RESULT 15  
US-10-098-263B-43779/c  
Sequence 43779, Application US/10098263B  
Publication No. US20030104410A1  
GENERAL INFORMATION:



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Page 1

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 00:43:42 ; Search time 2406 Seconds  
(without alignments)

248.231 Million cell updates/sec

Title: US-09-693-205A-47  
Perfect score: 20  
Sequence: 1 gtgaatgcacattgcact 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 22888

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:  
1: em\_estdb:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hnc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hnc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estum:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rnd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	11.8	59.0	24	28	AZ443113	IM0237G08
2	11.8	59.0	24	28	AZ498795	IM0336D16
3	11.6	58.0	19	28	AZ510142	IM0354P20
4	11.4	57.0	25	29	TA350F090	AL496767 T. brucei

C	5	11.2	56.0	25	9	AI344221	tc02h03.x
C	6	11.2	56.0	25	28	AZ510116	
C	7	10.4	52.0	20	28	AZ514794	IM0361C13
C	8	10.4	52.0	22	28	AZ794867	2M0048015
C	9	10.4	52.0	25	28	AZ404619	IM0173L20
C	10	10.4	52.0	25	29	TA237D08Q	
C	11	10.2	51.0	19	28	AZ358825	IM0101J20
C	12	10.2	51.0	19	28	AZ591963	IM0402P23
C	13	10.2	51.0	22	14	CF269578	FCY1C0Ld7
C	14	10.2	51.0	24	28	AZ837385	2M0132B10
C	15	10.2	51.0	25	28	AZ598351	IM0413D12
C	16	10.0	50.0	21	28	AZ552290	IM0090M10
C	17	9.8	49.0	20	28	AZ773092	IM0584K20
C	18	9.8	49.0	20	28	AZ784682	2M0027B07
C	19	9.8	49.0	21	28	AZ657958	IM0534E02
C	20	9.8	49.0	21	28	AZ814489	2M0082C14
C	21	9.6	48.0	20	28	AZ802430	2M0061C14
C	22	9.6	48.0	23	28	AQ934937	D11BGM68
C	23	9.6	48.0	25	28	AZ767331	IM0565N19
C	24	9.4	47.0	15	13	BQ511821	
C	25	9.4	47.0	19	28	AZ514722	IM0361C10
C	26	9.4	47.0	21	28	AZ447803	IM0245F08
C	27	9.4	47.0	21	28	AZ865515	2M0175U07
C	28	9.4	47.0	24	14	CA967214	CCLD1A03
C	29	9.4	47.0	24	29	TA100C01Q	
C	30	9.4	47.0	25	9	AA948130	0N51C12.s
C	31	9.4	47.0	25	9	AI181406	UC59404.r
C	32	9.2	46.0	20	9	AU255294	AU235294
C	33	9.2	46.0	20	28	AZ317291	IM0035N10
C	34	9.2	46.0	20	28	AZ630221	IM0483X12
C	35	9.2	46.0	20	28	AZ651800	IM0522N07
C	36	9.2	46.0	20	28	AZ662792	IM0542P02
C	37	9.2	46.0	20	28	AZ836069	2M0130J11
C	38	9.2	46.0	21	28	AZ836069	2M0130J11
C	39	9.2	46.0	21	28	AZ465773	AZ465773
C	40	9.2	46.0	22	28	AZ423553	IM0202N09
C	41	9.2	46.0	22	28	AZ949397	2M0212D23
C	42	9.2	46.0	23	28	AZ321517	IM042C12
C	43	9.2	46.0	23	28	AZ807926	2M0071C09
C	44	9.2	46.0	24	28	AZ845345	AZ845345
C	45	9.2	46.0	25	9	AI499484	tc02a09.x
C	46	9.2	46.0	25	9	AZ408539	IM0179G17

#### ALIGNMENTS

RESULT 1  
LOCUS AZ443113  
DEFINITION IM0237G08R Mouse 10kb plasmid UGCCIM library Mus musculus genomic clone UGCCIM0237G08 R, genomic survey sequence.  
ACCESSION AZ443113  
VERSION AZ443113.1 GI:10590773  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
MUS musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 24)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 306, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

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Email: ddum@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0237 row: G column: 08  
Seq primer: CACACGAGAAACACCTATGACC  
Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers

#### FEATURES

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGC1M037G08"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

#### ORIGIN

Query Match 59.0%; Score 11.8; DB 28; Length 24;  
Best Local Similarity 86.7%; Pred. No. 9.3e+04;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AATGCCACTTTGCA 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 4 AATGCCACTTTGAA 18

RESULT 2  
AZ498795 24 bp DNA linear GSS 05-OCT-2000  
LOCUS 1M0336D16F Mouse 10kb plasmid UGC1M library Mus musculus genomic  
DEFINITION clone UGC1M0336D16 F, genomic survey sequence.  
ACCESSION AZ498795  
VERSION AZ498795.1 GI:10676983  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 24)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddum@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0236 row: D column: 16  
Seq primer: CGTTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers

#### FEATURES

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

#### ORIGIN

Query Match 59.0%; Score 11.8; DB 28; Length 24;  
Best Local Similarity 86.7%; Pred. No. 9.3e+04;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AATGCCACTTTGCA 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 AATGCCACTTTGTA 15

RESULT 3  
AZ510142/c 19 bp DNA linear GSS 05-OCT-2000  
LOCUS 1M0354P20F Mouse 10kb plasmid UGC1M library Mus musculus genomic  
DEFINITION clone UGC1M0354P20 F, genomic survey sequence.  
ACCESSION AZ510142  
VERSION AZ510142.1 GI:10691458  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0354 row: P column: 20  
 Seq primer: CGTTGTAAACGACGGCCACT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers

#### FEATURES

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1.19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGGCM0354P20"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGGCM library"  
 /note="vector: pMD42nv; purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

#### ORIGIN

Query Match 58.0%; Score 11.6; DB 28; Length 19;  
 Best Local Similarity 77.8%; Pred. No. 1e+05;  
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 GTGAATGGCACTTGA 18  
 18 GTTAATGTCATCTGTA 1

#### RESULT 4

TA350F09Q 25 bp DNA linear GSS 13-DEC-2000  
 LOCUS T. brucei sheared genomic DNA clone 350F09, reverse sequence,  
 DEFINITION genomic survey sequence.  
 ACCESSION AL496767  
 VERSION AL496767.1 GI:11870376  
 KEYWORDS GSS.  
 SOURCE Trypanosoma brucei  
 ORGANISM Trypanosoma brucei  
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.  
 1 (bases 1 to 25)  
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
 Direct Submision  
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
 Cambridgeshire CB10 1SA, E-mail: barrell@sanger.ac.uk and  
 nhlesanger@sanger.ac.uk  
 Constructed at the Institute for Genomic Research (TIGR),  
 Rockville, MD. Genomic DNA isolated from a cloned population of  
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
 to give a tight size distribution (4 kb). The v + 1 method used for the library construction is  
 described in detail in Smith, H. and Venter, J.C. (Making small

#### COMMENT

#### JOURNAL

#### REFERENCE

AUTHORS

described in detail in Smith, H. and Venter, J.C. (Making small

Insert libraries for whole genome shotgun sequencing projects. In  
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
 Barrell, Oxford University Press, 1999).  
 Email: nhlesayer@tigr.org  
 Details of T. brucei sequencing at the Sanger Centre are available  
 at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).  
 Location/Qualifiers

#### FEATURES

source

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 /clone="J50F09"

#### ORIGIN

Query Match 57.0%; Score 11.4; DB 29; Length 25;  
 Best Local Similarity 92.3%; Pred. No. 1.5e+05;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 AATGCCCACTTTG 16  
 13 AATGCCCACTTTG 25

#### RESULT 5

AI144221/c 25 bp mRNA linear EST 08-APR-1999  
 LOCUS tco2h03.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:2062709 3'  
 DEFINITION similar to WP:CG95H.5 CB04231 ZINC-FINGER TRANSCRIPTION REGULATOR  
 ; mRNA sequence.

AI144221  
 AI144221.1 GI:4081427

#### ACCESSION

KEYWORDS

#### SOURCE

ORGANISM

#### REFERENCE

AUTHORS

#### JOURNAL

COMMENT

Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgsaps-remail.nih.gov  
 Tissue Procurement: Ian Kirsch, M.D., Michael R. Emmert-Buck,  
 M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
 www.bio.lnl.gov/bhrp/image/image.html

Trace considered overall poor quality  
 Insert Length: 462 Std Error: 0.00  
 Seq primer: -40UP from Gdbco  
 High quality sequence stop: 1.  
 Location/Qualifiers

#### FEATURES

source

1.25  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2062709"  
 /tissue\_type="colon tumor, RER+"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Col6"  
 /note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI;  
 Plasmid DNA from the normalized library NCI-CGAP Col6 was  
 prepared, and ss circles were made in vitro. Following HAP  
 purification, this DNA was used as tracer in a subtractive  
 hybridization reaction. The driver was PCR-amplified cDNAs  
 from a pool of 5,000 clones made from the same library

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SOURCE
1.23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCM0354H21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGGCM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1)", a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

```

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/organism="Mus musculus"
/mo_type="genomic DNA"
/strain="C57BL/6J"
/di_xref="taxon:10090"
/clone="TUGCIM0361C13"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid TUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g114732114[gb|AF12972.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

```

## ORIGIN

chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 52.0%; Score 10.4; DB 28; Length 20;  
Best Local Similarity 91.7%; Pred. No. 4.3e+05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATGGCCACTTTG 16  
DB 17 ATGGCCACTTGG 6

## RESULT 8

AZ794867 22 bp DNA linear GSS 16-FEB-2001

LOCUS 2M0048015R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0048015 R, genomic survey sequence.

DEFINITION AZ794867  
AZ794867  
AZ794867.1 GI:12941279

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0049 row: 0 column: 15  
Seq primer: CACACGAGAAACGCTACGACC  
Class: Plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

## FEATURES

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into

## ORIGIN

chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 52.0%; Score 10.4; DB 28; Length 22;  
Best Local Similarity 91.7%; Pred. No. 4.5e+05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TGGCCACTTGGC 17  
DB 6 TGGCCACTTGGC 17

## RESULT 9

AZ404619 25 bp DNA linear GSS 03-OCT-2000

LOCUS 1M0173J20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0173J20 F, genomic survey sequence.

DEFINITION AZ404619  
AZ404619  
AZ404619.1 GI:10528632

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 25)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0173 row: 1 column: 20  
Seq primer: CGTGTAAACGACGCGCCACG  
Class: Plasmid ends  
High quality sequence stop: 25.  
Location/Qualifiers

## FEATURES

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/clone="UUGC1M0173J20"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into





ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0402 row: P column: 23  
Seq primer: CGTGTAAACGACGCCACGT  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
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/db\_xref="taxon:10090"  
/clone="MUGC1M0402P23"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F."  
/clone\_lib="Mouse 10kb plasmid UGCM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (g14732114[gb]AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN  
Query Match 51.0%; Score 10.2; DB 28; Length 19;  
Best Local Similarity 80.0%; Pred. No. 5.3e+05;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 TGGCCACTTGGCACT 20  
|||||  
1 TGGCTACATTCCTCT 15

DB 1 TGGCTACATTCCTCT 15

RESULT 13  
CF269578 22 bp mRNA linear EST 13-AUG-2003  
CF269578  
DEFINITION Fcylcoid755 Fragilariopsis cylindrus SMART cDNA library (Clontech)  
ACCESSION CF269578  
VERSION CF269578.1 GI:33631465  
KEYWORDS EST.  
SOURCE Fragilariopsis cylindrus

ORGANISM Fragilariopsis cylindrus  
Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;  
Bacillariophycidae; Bacillariales; Bacillariaceae; Fragilariopsis.

REFERENCE 1 (bases 1 to 22)  
AUTHORS Mock, T. and Valentin, K.  
TITLE EST analysis of freezing tolerance in the Antarctic diatom  
Fragilariopsis cylindrus: Detection of numerous cold adaption  
related genes and gene transfer events  
JOURNAL Unpublished (2003)  
COMMENT Contact: Mock T  
Biological Oceanography  
Alfred-Wegener-Institute for Polar and Marine Research  
Am Handelshafen 12, D-27570 Bremerhaven, Germany  
Tel: +49 471 4831 1893  
Fax: +49 471 4831 1425  
Email: tmock@awi-bremerhaven.de  
sequence with unknown function  
PCR primers  
FORWARD: 5'lambdaT-IPLEX2  
BACKWARD: 3'lambdaT-IPLEX2  
Seq primer: ctgggaagcgcccatgtgtgtgtc.

FEATURES  
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/strain="Antarctic"  
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/clone="Antarctic"  
/clone\_lib="Fragilariopsis cylindrus SMART cDNA library  
(Clontech)"  
/note="Vector: Ptiplex2; total polyA was used for  
first-strand synthesis with SMART IV oligos and CDS  
III/3'PCR primer. Double strand cDNA synthesis was done by  
LD PCR using the following program: 95oc for 5 min  
denaturation and subsequent 20 cycles at 95oc (2min) and  
68oc (6min). After SfiI digestion the cDNA was  
fractionated with CHROMA Spin-400 columns. These cDNAs  
were ligated overnight into ptiplex2 vectors."

ORIGIN  
Query Match 51.0%; Score 10.2; DB 14; Length 22;  
Best Local Similarity 80.0%; Pred. No. 5.7e+05;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 TGGCCACTTGGCACT 20  
|||||  
1 TGGCCATTCGCCCT 15

DB 1 TGGCCATTCGCCCT 15

RESULT 14  
AZ837385 24 bp DNA linear GSS 20-FEB-2001  
AZ837385  
DEFINITION 2M0132E10R Mouse 10kb plasmid UGCM library Mus musculus genomic  
clone UGCM2M0132E10 R, genomic survey sequence.  
ACCESSION AZ837385  
VERSION AZ837385.1 GI:13007293  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0132 row: E column: 10  
Seq primer: CACACAGGAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 24.

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Location/Qualifiers  
1. .24

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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 51.0%; Score 10.2; DB 28; Length 24;  
Best Local Similarity 80.0%; Pred. No. 5.9e+05;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGAATGCCCACTTTG 16  
|||||  
Db 2 TGAATGCCCACTTTG 16

## RESULT 15

AZ598351  
LOCUS 1M0413D12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0413D12 F, genomic survey sequence.

ACCESSION AZ598351  
VERSION AZ598351.1 GI:11720541  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0413 row: D column: 12  
Seq primer: CGTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 25.

# FEATURES

Location/Qualifiers  
1. .25

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0413D12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 51.0%; Score 10.2; DB 28; Length 25;  
Best Local Similarity 80.0%; Pred. No. 6e+05;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGAATGCCCACTTTG 16  
|||||  
Db 2 TGAATGCCCACTTTG 16

Search completed: May 27, 2004, 02:22:36  
Job time : 2410 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

1 nucleic - nucleic search, using sw model

in on: May 26, 2004, 20:25:31 ; Search time 56.2249 Seconds  
(without alignments)  
4935.099 Million cell updates/sec

tle: US-09-693-205A-7\_COPY\_1\_500

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quence: 1 atgattacaggagaccat.....gcagaaattgtgtaatacaaa 500

oring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

sarched: 682709 seqs, 277475446 residues

tal number of hits satisfying chosen parameters: 1365418

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2\_6/ptodata/2/ina/5B COMB.seq:\*
- 3: /cgn2\_6/ptodata/2/ina/6A COMB.seq:\*
- 4: /cgn2\_6/ptodata/2/ina/6B COMB.seq:\*
- 5: /cgn2\_6/ptodata/2/ina/6C COMB.seq:\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
C 1	42.4	8.5	1407	4	US-09-328-352-1897
C 2	37.2	7.4	39003	4	US-09-596-002-21
C 3	36	7.2	1404	4	US-09-134-000C-2362
C 4	35.8	7.2	768	4	US-09-134-000C-1137
C 5	35.6	7.1	516	4	US-09-601-198-79
C 6	35.6	7.1	3129	3	US-09-387-695-1
C 7	35.6	7.1	19446	4	US-08-961-527-51
C 8	35.4	7.1	1664976	4	US-08-916-421B-1
C 9	35.2	7.0	832	4	US-09-621-976-2813
C 10	34.8	7.0	658	3	US-09-328-111-775
C 11	34.8	7.0	842	4	US-08-956-171B-808
C 12	34.2	6.8	3456	1	US-08-190-687B-24
C 13	34.2	6.8	4307	1	US-08-190-687B-7
C 14	34	6.8	392000	4	US-10-027-983-11
C 15	34	6.8	1664976	4	US-08-916-421B-1
C 16	33.6	6.7	819	4	US-09-601-198-45
C 17	33.6	6.7	1746	4	US-09-107-532A-3181
C 18	33.2	6.6	1308	4	US-09-601-198-3
C 19	33.2	6.6	5058	4	US-09-889-595-1
C 20	33.2	6.6	6479	2	US-08-649-046-3
C 21	33	6.6	1254	4	US-09-321-017B-1016
C 22	32.8	6.6	853	2	US-08-179-557-19
C 23	32.6	6.5	580073	4	US-08-545-528D-1
C 24	32.6	6.5	640681	4	US-09-790-988-1
C 25	32.4	6.5	279	4	US-09-601-198-25
C 26	32.4	6.5	501	4	US-09-328-352-3153
C 27	32.4	6.5	1590	4	US-09-403-942F-70

## ALIGNMENTS

### RESULT 1

US-09-328-352-1897/c  
; Sequence 1897, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:

; APPLICANT: Gary L. Breston et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 1897

; LENGTH: 1407  
; TYPE: DNA  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-1897

Query Match 8.5%; Score 42.4; DB 4; Length 1407;  
Best Local Similarity 54.5%; Pred. No. 0.0095;  
Matches 85; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY	306	TTTTAGACGATGTCGACGACGACGCTTCAGAAATTTTAGCAGACATGTCACAAAAC	365
Db	735	TTGGAAGCATGTAAACACAGGCATTCTGCATCAAAATCAGGAACCTTAAACTAAAC	676
QY	366	TTGGAGGCTTTTGCTCTTAAAAAATAGATGATCTATACACATCCGCTTATTAAAAAT	425
Db	675	TTGTAGGTTTGTGCTGACGCTCAAGTTTAAATTTCTGCTTCAGTCACTAAACCTAATGT	616
QY	426	ATATTCATTCACATTCACCAAGTCTCTTTTGCGA	461
Db	615	ACCTTCACCAACCAATAACAAATGCTGTAATGCATA	580

### RESULT 2

US-09-596-002-21  
; Sequence 21, Application US/09596002  
; Patent No. 6632636  
; GENERAL INFORMATION:

; APPLICANT: Lagace, Robert, E.  
; APPLICANT: Patterson, Chandra  
; APPLICANT: Berg, Kim, L.  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME  
; FILE REFERENCE: PM-0008-4 US  
; CURRENT APPLICATION NUMBER: US/09/596,002  
; CURRENT FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: 60/140,121  
; PRIOR FILING DATE: 1999-06-18  
; NUMBER OF SEQ ID NOS: 41

Sequence 71, Appl  
Sequence 67, Appl  
Sequence 69, Appl  
Sequence 1, Appl  
Sequence 4, Appl  
Sequence 4, Appl  
Sequence 13, Appl  
Sequence 18033, A  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 39, Appl  
Sequence 3940, Ap  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 1, Appl

```
; SOFTWARE: PERL Program
; SEQ ID NO 21
; LENGTH: 39003
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte template ID No. 6632636 21
; PUBLICATION INFORMATION:
; US-09-596-002-21

Query Match      7.4%; Score 37.2; DB 4; Length 39003;
Best Local Similarity 52.6%; Pred. No. 1;
Matches 81; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 291 TTCCATCGTTAGTCATTTTAGACGATGAATCTGAAGCACAGCTTCCAGAAATTTTAGCAG 350
Db 22598 TTATCTGGCTTGGCATCAAAACTCTGGTTTAAAGCACCTCTCCACAGTTTAAAGAAG 22657
QY 351 ACATTGTACAAAACCTTGGAGGGTTTGCTTTAAATAATTAGATGCTCTATACAAATC 410
Db 22658 AAGATGTTTAAATCTTAAATAAAATATCCTTAAATAAAATATCCTTAAATAAAATA 22717
QY 411 CGCTTATTAATAAATATATTCATTCACCAATACC 444
Db 22718 TCCTTAATAAATAATCTTAAATAAATAATC 22751

RESULT 3
US-09-134-000C-2362/c
; Sequence 2362, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2362
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
; US-09-134-000C-2362

Query Match      7.2%; Score 36; DB 4; Length 1404;
Best Local Similarity 53.6%; Pred. No. 0.66;
Matches 75; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 341 TTTTACGACATTTGTACAAAACCTGGAGGGTTTGCTTTAAAAAATTAGATGCATCT 400
Db 1199 TTTTACGCTTTCCATAATAAACTGAAGGGTTTATAAACACAAATATGGATGGAAT 1140
QY 401 ATACAACATCCGTTATTAATAAATATATTCATTCACCAATACCAAGTCTGTTTGCAG 460
Db 1139 GCATGGCTCAAACTAAATGATTAATTAATTCACCTTTAGTACCTCTTTAACAAG 1080
QY 461 ATATGAGAGATGCCATT 480
Db 1079 AATATGAATCAATAAATT 1060

RESULT 4
US-09-134-000C-1137
; Sequence 1137, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1137
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (311)..(311)
; OTHER INFORMATION: Nucleotide 311 is "n" wherein "n" = any nucleotide.
; US-09-134-000C-1137

Query Match      7.2%; Score 35.8; DB 4; Length 768;
Best Local Similarity 51.6%; Pred. No. 0.59;
Matches 82; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 305 ATTTTAGACGATGAATCTGAAGCACAGCTTCCAGAAATTTTAGCAGACATGTACAAAA 364
Db 430 ATTTTACATGGCTATACGAGAAAAACAGCAAGAAATTTGGAAACAAATTAACAAGCT 489
QY 365 CTGGAGGGTTTGCTTTAAAAAATTAGATGCATCTATACAAATCCGCTTATTAATAAAA 424
Db 490 GAACCAAGTTTGCTTTGTAGCATTTAGTTCCAGAAACAGAGAGATTTTGTGGACAA 549
QY 425 TATATTCATTCACCAATACCAAGTCTGTTTTCAGATA 463
Db 550 ACAATGTATCACCTGACAGCTAATGTATTTTAGACGTA 588

RESULT 5
US-09-601-198-79
; Sequence 79, Application US/09601198
; Patent No. 6531583
; GENERAL INFORMATION:
; APPLICANT: Cassell, Gail H.
; APPLICANT: Chen, Ellison Y.
; APPLICANT: Glass, Jennifer S.
; APPLICANT: Heiner, Cheryl R.
; APPLICANT: Lefkowitz, Elliot
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
; FILE REFERENCE: UAB-13452/22
; CURRENT APPLICATION NUMBER: US/09/601,198
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/073,189
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 79
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
; US-09-601-198-79

Query Match      7.1%; Score 35.6; DB 4; Length 516;
Best Local Similarity 48.5%; Pred. No. 0.58;
Matches 99; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 264 CATGTGTGAACATCATAGATTCAGATTCAGATTCATCGTTAGTCATTTTAGACGATGATCTG 323
Db 77 CAAGTGTGATTTAATTAATCATATGAAGAAATTAATGGCATCAGTTTATTTGATAATAAT 136
QY 324 AAGCAGAGCTTCCAGAAATTTTAGCAGACATGTACAAAACTTGGAGGGTTTGCCTTA 383
Db 137 TAGGTTTGAATCAGAGGTTTATTTAGATTTTGTCTTAAAAAATTTACATTAGCTTTTGAAA 196
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384 AAAAATAGATGATCTATACACATCCGCTTATTAAAAATATATTCATTCACCATTA 443  
197 AAAAATAGATGATCTATACACATCCGCTTATTAAAAATATATTCATTCACCATTA 256  
444 CAGTGTCTGTTTGCAGATAAT 465  
257 CCAACTATTAATGATCCAAAT 278

SULT 6  
-09-387-695-1/c  
Sequence 1, Application US/09387695  
Patent No. 6280990  
GENERAL INFORMATION:  
APPLICANT: May, Earl  
APPLICANT: Van Horn, Stephanie  
APPLICANT: Warren, Patrick V.  
APPLICANT: Warren, Richard L.  
TITLE OF INVENTION: dnae  
FILE REFERENCE: GM10237  
CURRENT APPLICATION NUMBER: US/09/387,695  
CURRENT FILING DATE: 1999-08-31  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 3129  
TYPE: DNA  
ORGANISM: Streptococcus pneumoniae  
;-09-387-695-1

Query Match 7.1%; Score 35.6; DB 3; Length 3129;  
Best Local Similarity 51.9%; Pred. No. 1.2;  
Matches 80; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

106 GATTGTTCAATGGTATCCATTTGATGAAACAGAAATCACCCATCTGTTTCATGGCTTAA 165  
2543 GATTCCTGCCAACTATAAATAGCATCTCCAAACAAACTTCCCAACTCTTTCACAAATTC 2484  
166 GATGTTTGGAAAAATCTTTATATACATTTTTCAGAGGATTTGACATTTATTTGATGAGAT 225  
2483 AATAGATTAGCTAAGTTATTAATACTTTTTCAGCATTTTTCATTAATGATGAGAT 2424  
226 GCACCTATCCCAAGCAATATCTAGAGGAGGT 259  
2423 CCAACTTTTACCAAGGTTCTAGCAGAGGAGGT 2390

3SULT 7  
-08-961-527-51/c  
Sequence 51, Application US/08961527  
Patent No. 6420135  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 391  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,527  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brooks, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PB340PI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19446 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: Double  
TOPOLOGY: linear  
US-08-961-527-51

Query Match 7.1%; Score 35.6; DB 4; Length 19446;  
Best Local Similarity 51.9%; Pred. No. 2.3;  
Matches 80; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

106 GATTGTTCAATGGTATCCATTTGATGAAACAGAAATCACCCATCTGTTTCATGGCTTAA 165  
17811 GATTCCTGCCAACTATAAATAGCATCTCCAAACAAACTTCCCAACTCTTTCACAAATTC 17752  
166 GATGTTTGGAAAAATCTTTATATACATTTTTCAGAGGATTTGACATTTATTTGATGAGAT 225  
17751 AATAGATTAGCTAAGTTATTAATACTTTTTCAGCATTTTTCATTAATGATGAGAT 17692  
226 GCACCTATCCCAAGCAATATCTAGAGGAGGT 259  
17691 CCAACTTTTACCAAGGTTCTAGCAGAGGAGGT 17658

RESULT 8  
US-08-916-421B-1  
Sequence 1, Application US/08916421B  
Patent No. 6503729  
GENERAL INFORMATION:  
APPLICANT: Bult et al.  
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus  
TITLE OF INVENTION: jannaschii  
Patent No. 6503729  
FILE REFERENCE: PB275  
CURRENT APPLICATION NUMBER: US/08/916,421B  
CURRENT FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: US 60/024,428  
PRIOR FILING DATE: 1996-08-22  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 1664976  
TYPE: DNA  
ORGANISM: Methanococcus jannaschii  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (28222)..(28222)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (28257)..(28258)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (84773)..(84773)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (84808)..(84808)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (84812)..(84812)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (98120)..(98120)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature

LOCATION: (98159)..(98159)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (98239)..(98239)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (98266)..(98266)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (98343)..(98343)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (10398)..(10398)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (148948)..(148948)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (163385)..(163385)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (191989)..(191989)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (191995)..(191995)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (231980)..(231980)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (234187)..(234187)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (234220)..(234220)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (234814)..(234814)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (309398)..(309398)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (309418)..(309418)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (312837)..(312837)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (312893)..(312893)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (319226)..(319226)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (559167)..(559167)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (559241)..(559241)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (600992)..(600992)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (622708)..(622708)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (657081)..(657081)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (657203)..(657203)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (674435)..(674435)

OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (682442)..(682442)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (713652)..(713652)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (741684)..(741684)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (779455)..(779455)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (779676)..(779676)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (855539)..(855539)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (871619)..(871619)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1084830)..(1084830)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1096846)..(1096846)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1119881)..(1119881)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1130881)..(1130881)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1310988)..(1310988)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1313224)..(1313224)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1349473)..(1349473)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1349491)..(1349491)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1470091)..(1470091)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1569020)..(1569020)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1602912)..(1602912)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1603734)..(1603734)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1637998)..(1637998)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1664854)..(1664854)  
OTHER INFORMATION: n equals a, t, c, or g  
US-08-916-421B-1

Query Match 7.1%; Score 35.4; DB 4; Length 1664976;  
Best Local Similarity 54.1%; Pred.No.14;  
Matches 72; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 102 AATTCATTGTTCAATGGTATCCATTGATGAAACAGAAATCACCCTCTGTTTCATGCG 161

DB 408286 AATAGATATGCTAACTATCCATTCGAGATTCAAAATGATCANTGTTTGTATC 408345





OPERATING SYSTEM: MSDOS version 6.12  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171E  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman  
REGISTRATION NUMBER: 46,789  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (240) 314-1224  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 808:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 842 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 808:  
US-08-956-171E-808

Query Match 7.0%; Score 34.8; DB 4; Length 842;  
Best Local Similarity 52.0%; Pred. No. 1.2;  
Matches 78; Conservative 0; Mismatches 72; Indels 0; Gaps 0;  
QY 351 ACATTGACAAAACCTGGAGGTTTGCCTTAAATAATTAGATGCATCATACAATC 410  
DB 734 ATATTTGCCAAAATAATTAAAGTTTCTATCTCTTTTATGATTTGATCTCTATTT 675  
QY 411 CGTTTATTAATAATATATTCATTCACCATTAACCAAGTCTGTTTTCAGATAATGGAGA 470  
DB 674 ATCTATAGATAATTTTATTTATTTTTCATTCACCTTTTATTAATTTTCTATCTGGAA 615  
QY 471 AGATGCCATTGCGAAATTTGTTATCAAA 500  
DB 614 TTGCCCCCTTATTATAGATGTTCTTAACAA 585

RESULT 12  
US-08-190-687B-24  
Sequence 24, Application US/08190687B  
Patent No. 5760203  
GENERAL INFORMATION:  
APPLICANT: Wong, Gail L.  
APPLICANT: Martin, George  
APPLICANT: McCormick, Francis P.  
APPLICANT: Rubinfeld, Bonnie  
APPLICANT: O'Rourke, Edward C.  
APPLICANT: Clark, Robin  
TITLE OF INVENTION: GAP Gene Sequences  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/190,687B  
FILING DATE: 02-FEB-1994  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/774,644  
FILING DATE: 11-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/260,807  
FILING DATE: 21-OCT-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/230,761  
FILING DATE: 10-AUG-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 27527/31898  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3456 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 100..2709  
US-08-190-687B-24  
Query Match 6.8%; Score 34.2; DB 1; Length 3456;  
Best Local Similarity 55.5%; Pred. No. 3;  
Matches 66; Conservative 0; Mismatches 53; Indels 0; Gaps 0;  
QY 343 TTATACACACATTTTACAAAACCTGGAGGTTTGCCTTAAATAATTAGATGCATCTAT 402  
DB 2100 TTATACACACATTTTGAACATATTCAGACCTTGTGGAGAAATATTCATGCGTTTCA 2159  
QY 403 ACAACATCGCTTATTAATAATAATATTCATTCACCATTAACCAAGTCTGTTTTCGAGA 461  
DB 2160 AATACTTCCACGACATTGAGATATATTTATGGTGTTTACAGAAATCTGTTACGATA 2218  
RESULT 13  
US-08-190-687B-7  
Sequence 7, Application US/08190687B  
Patent No. 5760203  
GENERAL INFORMATION:  
APPLICANT: Wong, Gail L.  
APPLICANT: Martin, George  
APPLICANT: McCormick, Francis P.  
APPLICANT: Rubinfeld, Bonnie  
APPLICANT: O'Rourke, Edward C.  
APPLICANT: Clark, Robin  
TITLE OF INVENTION: GAP Gene Sequences  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/190,687B  
FILING DATE: 02-FEB-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/774,644

FILING DATE: 11-OCT-1991  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/260,807  
FILING DATE: 21-OCT-1988  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/230,761  
FILING DATE: 10-AUG-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 27527/31898  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
LENGTH: 4307 base pairs  
TYPE: nucleic acid  
STRADEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

NAME/KEY: CDS  
LOCATION: 119..3259  
S-08-190-687B-7

Query Match 6.8%; Score 34.2; DB 1; Length 4307;  
Best Local Similarity 55.5%; Pred. No. 3.3;  
Matches 66; Conservative 0; Mismatches 53; Indels 0; Gaps 0;  
y 343 TTACGACATGTTACAAAACCTGGAGGGTTTCCTTAAAAAATTAGATCATCTAT 402  
b 2650 TTAAACACACCTATTGAACATCTTTCAGAGCTTGGAGAAATATTCATGGCTTCAGA 2709  
y 403 ACACATCGCTTATTAAAAAATATTCATTCACCATACCAAGTCTGTTTGCAGA 461  
b 2710 AATCTCCACCGACATTGAGATATATTATGGGTGTTTACAGAAATCTGTTACGACATA 2768

ESULT 14  
S-10-027-983-11/c  
Sequence 11. Application US/10027983  
Patent No. 6617162  
GENERAL INFORMATION:  
APPLICANT: Kenneth W. Dobie  
APPLICANT: Mark P. Roach  
TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR ALPHA EXPRESSION  
FILE REFERENCE: RTS-0340  
CURRENT APPLICATION NUMBER: US/10/027,983  
CURRENT FILING DATE: 2001-12-18  
NUMBER OF SEQ ID NOS: 98  
SEQ ID NO 11  
LENGTH: 392000  
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ORGANISM: Homo sapiens  
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US-10-027-983-11

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Best Local Similarity 57.5%; Pred No. 21;
Matches 61; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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DB 359266 AATGTTATTATATATATCCCTGGAAGAGAAATCACTTACGCTGTTTACACATCAGATTTGTT 359207

QY 174 GGAATAATCTTTATATACATATTTTCAGAGGATTTGACTTTATTGGA 219
DB 359206 GAATAAATCATCTTTGATCAATCATCATCTGATATATAGTTATTAA 359161

RESULT 15
US-08-916-421B-1/c
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; Patent No. 6503729
; FILE OF INVENTION: jannaschii
; TITLE OF INVENTION: jannaschii
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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; ORGANISM: Methanococcus jannaschii
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S-08-916-421B-1

Query Match 6.8%; Score 34; DB 4; Length 1664976;  
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y 332 CTTCCAGAAATTTTACACACATTTGACAAAACCTTGAGGGTTTGCTTAAAAAATTA 391  
b 74997 AATTAGATGATTTTGGAGAAGTATCAACAAGCTTCAATAGCTTAGGCTTTAAAAAAGTT 74938  
y 392 GATGCATCTATCAACATCGCTTATTAATAATATTCAT 433  
b 74937 GAACCTCTTTACATCAGATATTGTTAAGATTAAATAT 74896

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GenCore version 5.1.6  
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4 nucleic - nucleic search, using sw model

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searched: 2953838 seqs, 2272363821 residues

total number of hits satisfying chosen parameters: 5907676

inimum DB seq length: 0  
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
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- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
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- 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	424	84.8	11490	13	US-10-342-887-1480
2	424	84.8	11490	13	US-10-172-118-1480
3	40	8.0	1048	13	US-10-027-632-245140
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5	39.4	7.9	2000	9	US-09-938-842A-5280
6	39.4	7.9	2000	11	US-09-938-842A-5280
7	38.4	7.7	3673778	15	US-10-312-841-2
8	37.8	7.6	312	9	US-09-969-373-349
9	37.8	7.6	513509	10	US-09-754-853A-4
10	37.4	7.5	646	9	US-09-770-149-579
11	37.4	7.5	1227	13	US-10-282-122A-18133
12	37.4	7.5	11172	15	US-10-311-455-2026
13	37.2	7.4	1140	13	US-10-027-632-117466
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c 18	37.2	7.4	3129	13	US-10-282-122A-37729
c 19	37.2	7.4	30277	13	US-10-087-192-1201
c 20	37.2	7.4	39003	13	US-10-672-787-21
c 21	37.2	7.4	40862	15	US-10-311-455-2046
c 22	36	7.2	829	13	US-10-424-599-48972
c 23	36	7.2	11410	9	US-09-070-927A-190
c 24	35.8	7.2	744	13	US-10-282-122A-20933
c 25	35.6	7.1	516	15	US-10-349-680-17
c 26	35.6	7.1	3129	9	US-09-925-697-1
c 27	35.6	7.1	7231	15	US-10-240-452-23
c 28	35.6	7.1	19446	13	US-10-158-844-51
c 29	35.4	7.1	878	16	US-10-027-632-171302
c 30	35.4	7.1	1081	15	US-10-017-161-2367
c 31	35.4	7.1	6210	15	US-10-240-453-345
c 32	35.4	7.1	591	13	US-10-027-632-21675
c 33	35.2	7.0	591	16	US-10-027-632-21675
c 34	35.2	7.0	668	13	US-10-027-632-106284
c 35	35.2	7.0	668	16	US-10-027-632-106284
c 36	35.2	7.0	824	13	US-10-027-632-127339
c 37	35.2	7.0	824	13	US-10-027-632-127340
c 38	35.2	7.0	824	16	US-10-027-632-127339
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c 40	35.2	7.0	2066	10	US-09-814-353-20027
c 41	35.2	7.0	2226	13	US-10-424-599-98187
c 42	35.2	7.0	3034	13	US-10-116-802-424
c 43	35.2	7.0	684707	16	US-10-398-221-9
c 44	35.2	7.0	3011208	16	US-10-398-221-2058

ALIGNMENTS

RESULT 1

US-10-342-887-1480  
; Sequence 1480, Application US/10342887  
; Publication No. US20040058340A1  
; GENERAL INFORMATION:  
; APPLICANT: Dai, Hongyue  
; APPLICANT: He, Yundong  
; APPLICANT: Linsley, Peter S.  
; APPLICANT: Mao, Mao  
; APPLICANT: Roberts, Christopher J.  
; APPLICANT: Van 't Veer, Laura Johanna  
; APPLICANT: Van de Vijver, Marc J.  
; APPLICANT: Bernards, Rene  
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
; FILE REFERENCE: 9301-188-999  
; CURRENT APPLICATION NUMBER: US/10/342,887  
; CURRENT FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: 60/298,918  
; PRIOR FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 60/380,710  
; PRIOR FILING DATE: 2002-05-14  
; PRIOR APPLICATION NUMBER: 10/172,118  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 2699  
; SEQ ID NO 1480  
; LENGTH: 11490  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-342-887-1480

Query Match 84.8%; Score 424; DB 13; Length 11490;  
Best Local Similarity 100.0%; Pred. No. 3.8e-101;  
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 ATGAATACATCTGGCTGGCAGAGAAATGATGTTGATCCATTCATTCATGAAC 60

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 497 CAAA 500  
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RESULT 2

US-10-172-118-1480  
 ; Sequence 1480, Application US/10172118  
 ; Publication No. US20030224374A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dai, Hongyue  
 ; APPLICANT: He, Yudong  
 ; APPLICANT: Linsley, Peter  
 ; APPLICANT: Mao, Mao  
 ; APPLICANT: Roberts, Chris  
 ; APPLICANT: Van 't Veer, Laura  
 ; APPLICANT: Van de Vijver, Marc  
 ; APPLICANT: Bernards, Rene  
 ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
 ; FILE REFERENCES: 9301-175-999  
 ; CURRENT APPLICATION NUMBER: US/10/172,118  
 ; CURRENT FILING DATE: 2002-06-14  
 ; PRIOR APPLICATION NUMBER: 60/380,770  
 ; PRIOR FILING DATE: 2002-05-14  
 ; NUMBER OF SEQ ID NOS: 2699  
 ; SEQ ID NO 1480  
 ; LENGTH: 11490  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; PUBLICATION INFORMATION:  
 ; DATABASE ACCESSION NUMBER: NM\_014363  
 ; DATABASE ENTRY DATE: 2001-06-18  
 US-10-172-118-1480

Query Match 84.8%; Score 424; DB 13; Length 11490;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-101; Indels 0; Gaps 0;  
 Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 77 ATGAATACATCTTGGCTGSCAGAGAAATGATTTCAATGGTATCCATTTGATGAAGAAAC 136  
 1 ATGAATACATCTTGGCTGSCAGAGAAATGATTTCAATGGTATCCATTTGATGAAGAAAC 60  
 137 AGAATCACCACCTGTTTCATGGCTTAAGATGGTTTGGAAAAATCTTTATATACATTTT 196  
 61 AGAATCACCACCTGTTTCATGGCTTAAGATGGTTTGGAAAAATCTTTATATACATTTT 120  
 197 TCAGAGGATTTGACCTTTATTTGATGAGATGGCACTATATCCCGAAGACTATATAGAGGAA 256

121 TCAGAGGATTTGACCTTTATTTGATGAGATGCCATTTATCCCGAAGACTATATAGAGGAA 180  
 257 GGTACAGATGTTGGAACTCATTAGACTCAGGATTCATCGTTAGTCAATTTAGACGAT 316  
 181 GGTACAGATGTTGGAACTCATTAGACTCAGGATTCATCGTTAGTCAATTTAGACGAT 240  
 317 GAATCTGAAGCAGCTTCCAGAAATTTTAGCAGACATTTGACAGAACTTTGGAGGGTTT 376  
 241 GAATCTGAAGCAGCTTCCAGAAATTTTAGCAGACATTTGACAGAACTTTGGAGGGTTT 300  
 377 GTCCCTTAAAAAATAGATCCTATACAACTCGCTTATTAATAATATATATTCATCA 436  
 301 GTCCCTTAAAAAATAGATCCTATACAACTCGCTTATTAATAATATATATTCATCA 360  
 437 CCATTACCAAGTCTGTTTTCAGATAATGGAGAGATGCCATTGCAGAAATTTGTGAAT 496  
 361 CCATTACCAAGTCTGTTTTCAGATAATGGAGAGATGCCATTGCAGAAATTTGTGAAT 420  
 497 CAAA 500  
 421 CAAA 424

RESULT 3

US-10-027-632-245140/c  
 ; Sequence 245140, Application US/10027632  
 ; Publication No. US20020198371A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome  
 ; FILE REFERENCES: 108827.129  
 ; CURRENT APPLICATION NUMBER: US/10/027,632  
 ; CURRENT FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/218,006  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/198,676  
 ; PRIOR FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/193,483  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: US 60/185,218  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/167,363  
 ; PRIOR FILING DATE: 1999-11-23  
 ; PRIOR APPLICATION NUMBER: US 60/156,358  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/146,002  
 ; PRIOR FILING DATE: 1999-08-09  
 ; NUMBER OF SEQ ID NOS: 325720  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 245140  
 ; LENGTH: 1048  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-10-027-632-245140

Query Match 8.0%; Score 40; DB 13; Length 1048;  
 Best Local Similarity 52.4%; Pred. No. 3.6;  
 Matches 88; Conservative 0; Mismatches 80; Indels 0; Gaps 0;  
 104 TTGATTGTTCAATGGTATCCATTTGATGAAGAAATCACCATCTCTGTTTCATGGCTT 163  
 924 TTGATATAGAAGCAGTCCATTTGACCTTACAGAAACCCACCAATTTTTTTTATCAAA 865  
 164 AGATGGTTTGGAAAAATCTTTATATACATTTTTCAGAGGATTTGACCTTTATTTGATGAG 223  
 864 AACACAATATTCATCTGTCTCAATATAAACTTTGATAAAGATGTGACATGACAGAGTTG 805  
 224 ATGCCACTTATCCCGAAGACTATATAGAGAGAGGTGCAGACATGTGTG 271  
 804 AGACACTAGTTCAAGTCAATGTCCTCCAGACATCTCTTCAGAAATTTATG 757

SULT 4  
-10-027-632-245140/c  
Sequence 245140, Application US/10027632  
Publication No. US20030204075A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027.632  
CURRENT FILING DATE: 2002-04-30  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 245140  
LENGTH: 1048  
TYPE: DNA  
ORGANISM: Human  
;-10-027-632-245140  
Query Match 8.0%; Score 40; DB 16; Length 1048;  
Best Local Similarity 52.4%; Pred. No. 3.6;  
Matches 88; Conservative 0; Mismatches 80; Indels 0; Gaps 0;  
104 TTGATTGTTCAATGCTATCCATTTGATGAAACAGAAATCCACCATCTGTTTCATGGCTT 163  
924 TTGGATATAGAAAGCAGTCCTTACGATTTTACGAAACACCAATTTTTCATCAAA 865  
164 AGATGGTTTGAAGAAATCTTTATATACATTTTTCAGAGGATTTGATTTATTTGATGAG 223  
864 AACACAAATTTCTCTGTCCTTCAATTAATTAATTTGATAGAAATGTCATGACAGAGTTG 805  
224 ATGCCACTTATCCCGAAGCTATATCTAGAGGAAGTCCAGCATGTGTG 271  
804 AGACACTAGTTCAAAGTCAATGCTCCAGACATTTCTTCAGAAATTTATG 757  
35ULT 5  
3-09-938-842A-5280  
Sequence 5280, Application US/09938842A  
Patent No. US20030160378A1  
GENERAL INFORMATION:  
APPLICANT: Harper, Jeff  
APPLICANT: Kreps, Joel  
APPLICANT: Wang, Xun  
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
THE SAME, AND METHODS OF USE  
FILE REFERENCE: SRIPI300-3  
CURRENT APPLICATION NUMBER: US/09/938,842A  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: US 60/227,866  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/264,647  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/300,111  
PRIOR FILING DATE: 2001-06-22  
NUMBER OF SEQ ID NOS: 5379  
SEQ ID NO 5280  
LENGTH: 2000  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-938-842A-5280  
Query Match 7.9%; Score 39.4; DB 11; Length 2000;  
Best Local Similarity 61.0%; Pred. No. 7.3;  
Matches 64; Conservative 0; Mismatches 41; Indels 0; Gaps 0;  
115 ATGGTATCCATTTGATGAAACAGAAATCCACCATCTGTTTCATGGCTTAAGATGTTTG 174  
93 AGGGTATCAAAATTAAGAAATGTACATTTTATAAAATTTTCAAGGCTTTTATGTTTA 152  
175 GAAAAATCTTTATATACATTTTTCAGAGGATTTGACTTTATTGGA 219  
153 AGAAAAATATTATACGCATTTTATTAATAAATTCATTTTGTGGA 197  
RESULT 6  
US-09-938-842A-5280  
Sequence 5280, Application US/09938842A  
Publication No. US20040009476A9  
GENERAL INFORMATION:  
APPLICANT: Harper, Jeff  
APPLICANT: Kreps, Joel  
APPLICANT: Wang, Xun  
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
THE SAME, AND METHODS OF USE  
FILE REFERENCE: SRIPI300-3  
CURRENT APPLICATION NUMBER: US/09/938,842A  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: US 60/227,866  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/264,647  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/300,111  
PRIOR FILING DATE: 2001-06-22  
NUMBER OF SEQ ID NOS: 5379  
SEQ ID NO 5280  
LENGTH: 2000  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-938-842A-5280  
Query Match 7.9%; Score 39.4; DB 11; Length 2000;  
Best Local Similarity 61.0%; Pred. No. 7.3;  
Matches 64; Conservative 0; Mismatches 41; Indels 0; Gaps 0;  
115 ATGGTATCCATTTGATGAAACAGAAATCCACCATCTGTTTCATGGCTTAAGATGTTTG 174  
93 AGGGTATCAAAATTAAGAAATGTACATTTTATAAAATTTTCAAGGCTTTTATGTTTA 152  
175 GAAAAATCTTTATATACATTTTTCAGAGGATTTGACTTTATTGGA 219  
153 AGAAAAATATTATACGCATTTTATTAATAAATTCATTTTGTGGA 197  
RESULT 7  
US-10-312-841-2/c  
Sequence 2, Application US/10312841  
Publication No. US20030186277A1  
GENERAL INFORMATION:  
APPLICANT: Epigenomics AG  
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC  
FILE REFERENCE: E01/1208/WO  
CURRENT APPLICATION NUMBER: US/10/312,841  
CURRENT FILING DATE: 2002-12-30  
NUMBER OF SEQ ID NOS: 2  
SEQ ID NO 2  
LENGTH: 3673778  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (379615)  
US-10-312-841-2

Query Match 7.6%; Score 38.4; DB 15; Length 3673778;  
Best Local Similarity 47.9%; Pred. No. 5.1e+02;  
Matches 140; Conservative 0; Mismatches 151; Indels 1; Gaps 1;  
QY 172 TTGGAAAAATCTTTATATACATTTTTCAGAGGATTTGACCTTTTATTTGAGATGCCACT 231  
DB 845551 TTTTAAACCTTAAATAATATCTTTATACATTTCTAATTTTCAAAAATTCCTT 845492  
QY 232 TATCCCGAAGACTACTACT-AGAGGAGGTCAGACATGTGTGGAACTCATTTAGACTCAGA 290  
DB 845491 CATCACCATAATTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 845432  
QY 291 TTCCATCGTTAGTCAATTTTATAGCATGATCTGGAAGCAGACAGCTTCCAGAAATTTTAGCAG 350  
DB 845431 ATCCATTAATCT 845372  
QY 351 ACATTTGTCAAAAACTTGGAGGTTTGTCTTAAAAAATAGATGCATCTATACATC 410  
DB 845371 TCACCACATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 845312  
QY 411 CGTTTATTAATAATAATATCTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 462  
DB 845311 AATATCTAAATCAATTAATAAAAAAACTTCAAACTTATTTATATATAAT 845260

RESULT 8  
US-09-969-373-349/c  
Sequence 349, Application US/09969373  
Patent No. US2002013852A1  
GENERAL INFORMATION:  
APPLICANT: Haug, Brian M.  
APPLICANT: Eifert, Roger J.  
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
FILE REFERENCE: 38-10(52679)A  
CURRENT APPLICATION NUMBER: US/09/969,373  
CURRENT FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: US 09/754,853  
PRIOR FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: US 09/760,427  
PRIOR FILING DATE: 2001-01-13  
PRIOR APPLICATION NUMBER: US 09/855,768  
PRIOR FILING DATE: 2001-05-15  
NUMBER OF SEQ ID NOS: 4593  
SEQ ID NO 349  
LENGTH: 312  
TYPE: DNA  
ORGANISM: Glycine max  
US-09-969-373-349

Query Match 7.6%; Score 37.8; DB 9; Length 312;  
Best Local Similarity 48.4%; Pred. No. 7.3; Indels 0; Gaps 0;  
Matches 105; Conservative 0; Mismatches 112  
QY 178 AAATCTTTATATACATTTTTCAGAGGATTTGACCTTTTATTTGATGAGATGCCACTTATCCC 237  
DB 297 AATTATGTAAATAATATATAGATTAATTAATTAAGAAATAATATGATATGCTAATGATAA 238  
QY 238 CAGAACTATCTAGAGGAGGTCAGACATGTGTGGAACTCATTTAGACTCAGATTCATC 297  
DB 237 ATATAATTTTATATCACTATATAATTTATTTATTTATTTATTTATTTATTTATTTATC 178  
QY 298 GTTAGTCAATTTTATAGCATGATCTGGAAGCAGACAGCTTCCAGAAATTTTAGCAGCATGT 357  
DB 177 ATAAATCAATATATATGATCAATTTTCTGAACTTTTATATAAAAAAACTACTTTAAAAAGT 118  
QY 358 AAAAAAATTTGGAGGTTTGTCTTAAAAAATTAGAT 394

Db 117 ACATTAATGTGATTTTATTTATTTGATCGACATTTGTAAT 81  
RESULT 9  
US-09-754-853A-4/c  
Sequence 4, Application US/09754853A  
Publication No. US20030005491A1  
GENERAL INFORMATION:  
APPLICANT: Haug, Brian M.  
APPLICANT: Parsons, Jeremy D.  
APPLICANT: Wang, Ming Li  
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
FILE REFERENCE: 38-10(11810)B  
CURRENT APPLICATION NUMBER: US/09/754,853A  
CURRENT FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: US 60/174,880  
PRIOR FILING DATE: 2000-01-07  
NUMBER OF SEQ ID NOS: 1119  
SEQ ID NO 4  
LENGTH: 513509  
TYPE: DNA  
ORGANISM: Glycine max  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (111805)..(113968), (114684)..(115204)  
NAME/KEY: unsure  
LOCATION: (1)..(513509)  
OTHER INFORMATION: unsure at all n locations  
OTHER INFORMATION: Clone ID: 318013\_region\_A3  
US-09-754-853A-4  
Query Match 7.6%; Score 37.8; DB 10; Length 513509;  
Best Local Similarity 48.4%; Pred. No. 3.4e+02;  
Matches 105; Conservative 0; Mismatches 112; Indels 0; Gaps 0;  
QY 178 AAATCTTTATATACATTTTTCAGAGGATTTGACCTTTTATTTGATGAGATGCCACTTATCCC 237  
DB 477427 AATTATGTAAAAATATATATAGATTAATTTAAGAAAAATAATGATGCTAATGATAA 477368  
QY 238 CAGAACTATCTAGAGGAGGTCAGACATGTGTGGAATCTATTAGACTCAGATTCATC 297  
DB 477367 ATATTAATTTTATATCACTATATATTTTATTTATTTATTTATTTATTTATTTATC 477308  
QY 298 GTTAGTCAATTTTATAGCATGATCTGGAAGCAGACAGCTTCCAGAAATTTTAGCAGCATGT 357  
DB 477307 ATAAATCAATATATATGATCAATTTTACTGAACTTTTATAAAAAAACTACTTTAAAAAGT 477248  
QY 358 AAAAAAATTTGGAGGTTTGTCTTAAAAAATTAGAT 394  
DB 477247 ACATTAATGTGATTTTATTTATTTGATCGACATTTGTAAT 477211

RESULT 10  
US-09-770-149-579/c  
Sequence 579, Application US/09770149  
Patent No. US2002005963A1  
GENERAL INFORMATION:  
APPLICANT: Gorlach, Jörn  
APPLICANT: An, Yong-Qiang  
APPLICANT: Hamilton, Carol M.  
APPLICANT: Price, Jennifer L.  
APPLICANT: Raines, Tracy M.  
APPLICANT: Yu, Yang  
APPLICANT: Rameaka, Joshua G.  
APPLICANT: Page, Amy  
APPLICANT: Matthew, Abraham V.  
APPLICANT: Ledford, Brooke L.  
APPLICANT: Woessner, Jeffrey P.  
APPLICANT: Haas, William David  
APPLICANT: Garcia, Carlos A.



APPLICANT: Krickler, Maja  
APPLICANT: Slader, Ted  
APPLICANT: Davis, Keith R.  
APPLICANT: Allen, Keith  
APPLICANT: Hoffman, Neil  
APPLICANT: Hurban, Patrick  
TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
FILE REFERENCE: thaliana  
CURRENT APPLICATION NUMBER: US/09/770,149  
CURRENT FILING DATE: 2001-01-26  
PRIORITY APPLICATION NUMBER: 60/178,506  
PRIORITY FILING DATE: 2000-01-27  
NUMBER OF SEQ ID NOS: 999  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 579  
LENGTH: 646  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
S-09-770-149-579

Query Match 7.5%; Score 37.4; DB 9; Length 646;  
Best Local Similarity 48.8%; Pred. No. 14;  
Matches 101; Conservative 0; Mismatches 106; Indels 0; Gaps 0;  
Y 222 AGATGCCATTATCCCGAGACTATAGAGGAGGTCAGACATGTGTGGAACCTCATTA 281  
b 233 AGATCCCGCTTAGGCTGTAGTGAGTAAAGGCGAGATGTGTAAAGAAAAA 174  
Y 282 GACTCAGGATTCATCGTTAGTCATTTTAGACGATGAATCTGAAGCAGCTTCAGAAAT 341  
b 173 TGTGTAGGATTTTAGAGTTTTCCTTTCATGTACAAAAAGATGGCTCTTACGCCAAT 114  
Y 342 TTTTAGAGACATGTACAAAAACCTTGGAGGTTTGTCTTTAAAAAATAGATGATCTA 401  
b 113 GTGTAGATGCTTTTGTAGAACATCCAGCTTTATTTCAGTATAAAAAATAAAAAA 54  
Y 402 TACAACATCGCTTATTAAAAAATA 428  
b 53 AAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 11  
S-10-282-122A-18133/c  
Sequence 18133, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Olsen, Kari  
APPLICANT: Zykkind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIORITY APPLICATION NUMBER: 60/191,078  
PRIORITY FILING DATE: 2000-03-21  
PRIORITY APPLICATION NUMBER: 60/206,848  
PRIORITY FILING DATE: 2000-05-23  
PRIORITY APPLICATION NUMBER: 60/207,727  
PRIORITY FILING DATE: 2000-05-26  
PRIORITY APPLICATION NUMBER: 60/230,335  
PRIORITY FILING DATE: 2000-09-06  
PRIORITY APPLICATION NUMBER: 60/230,347  
PRIORITY FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-03-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 18133  
LENGTH: 1227  
TYPE: DNA  
ORGANISM: Campylobacter jejuni  
US-10-282-122A-18133  
Query Match 7.5%; Score 37.4; DB 13; Length 1227;  
Best Local Similarity 44.6%; Pred. No. 19;  
Matches 146; Conservative 0; Mismatches 181; Indels 0; Gaps 0;  
QY 146 CCATCTGTTTCATGCTTAAGATGGTTTGGAAAAATCTTTATATACATTTTCAGAGAT 205  
Db 1021 CCAATTCITTTAGCAAAATGATAAATTATTGGCAAAATGACGATTTGGATTTGTATAAAT 962  
QY 206 TTGACTTTTATTTGATGAGTGCCTTATCCCGAAGTACTATAGAGGAGGTCAGACA 265  
Db 961 ATACAAATTAATTTAGTAGGAGGATTAAGATGACAAATATCAAAAAATTTATAGAC 902  
QY 266 TGTGTGGAACTCATTAGACTCAGGATTCCTGTTAGTCAATTTTAGACGATGAATCTGAA 325  
Db 901 ATCTATAAGATTTTATACCTTAATCGAAAACTAGTAATCTCACCCCTATACTTTGCA 842  
QY 326 GCACACTTCCAGAAATTTTAGCAGACATTTGACAAAACTTGGAGGTTTGTCTTTAAA 385  
Db 841 TTAAGTTTATAGCAAGGAGTGCACAAATTAACAAAAAGGCAAAAAATCATCTAAA 782  
QY 386 AAATTAGATGCATCTATACACATCCGCTTTATTAATAAATATATTTCATTCCACATTACCA 445  
Db 781 AAAGTTTGTCTTAAAGAACACAAACAAATGATTTACGCTCATTTAAACC 722  
QY 446 AGTGTGTTTTCAGATTAATGGAGAAG 472  
Db 721 ATAATAAATTTTATATTTTGGAAAG 695

RESULT 12  
US-10-311-455-2026/c  
Sequence 2026, Application US/10311455  
Publication No. US20030143606A1  
GENERAL INFORMATION:  
APPLICANT: OLEK, Alexander  
APPLICANT: PIEPENBROCK, Christian  
APPLICANT: BERLIN, Kurt  
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ  
TITLE OF INVENTION: cytosine methylation  
FILE REFERENCE: 5013.1014  
CURRENT APPLICATION NUMBER: US/10/311,455  
CURRENT FILING DATE: 2002-12-16  
PRIOR APPLICATION NUMBER: PCT/EP01/07537  
PRIOR FILING DATE: 2001-07-02  
PRIOR APPLICATION NUMBER: DE 10032529.7  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: DE 10043826.1  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 2424  
SEQ ID NO 2026  
LENGTH: 11172  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-311-455-2026

Query Match 7.5%; Score 37.4; DB 15; Length 11172;  
Best Local Similarity 53.8%; Pred. No. 60;  
Matches 77; Conservative 0; Mismatches 66; Indels 0; Gaps 0;  
QY 299 TTAGTCATTTTACAGCATGAATCTGAAGCACAGCTCCAGAAATTTTACGACAGATTGTA 358  
Db 9356 TAAATCACCTTAATCATATAAATCTATAATCCATTTTAAATATTTTATAAAAAATATAA 9297  
QY 359 CAAAAACTGGAGGGTTCTCTTAAAAATAGATGATCATACACATCCCGCTTATT 418  
Db 9296 AATTACGTTAAATTTATTTTATCTTTTAAATATCCAAATTTTCAATAACTATTATT 9237  
QY 419 AAAAAATATATTCATTCACATT 441  
Db 9236 AAAAAAATCTATCTTCCATTATT 9214

RESULT 13  
US-10-027-632-117466/c  
; Sequence 117466, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 117466  
; LENGTH: 1140  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(1140)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-027-632-117466

Query Match 7.4%; Score 37.2; DB 13; Length 1140;  
Best Local Similarity 49.0%; Pred. No. 21;  
Matches 96; Conservative 1; Mismatches 99; Indels 0; Gaps 0;  
QY 2 TGATTTACAGGAAGACCATGATCTAGCTGCAGCTTCTTAAATCCAGAACGATTTCACGT 61  
Db 616 TGTTTTGTGTTGAATAACATAAAATATTTAAAGTCTCTAATAGTTCATTGTAAGAAAGG 557  
QY 62 CTTATCAGGAAGTAATGAATACATTTCTGGCTGCGAGAGATTTGTTCAATGGTAT 121  
Db 556 CTAATGAGAAATTTGTTAGGACATAGTACACACTGAATGTAGATGCTRT 497  
QY 122 CCATTTGATGAACAGAAATCAATCCATCTGTTTCATGCTTAAGATGTTTGGAAAAAT 181  
Db 496 AAACATAAGCCAGCAAGAACGACATTTATTAGATGTTAGTCTACTTCTCGGAGGAT 437

QY 182 CTTTATATACATTTT 197  
Db 436 TTTTGTCTTCTATATT 421  
RESULT 14  
US-10-027-632-117467/c  
; Sequence 117467, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 117467  
; LENGTH: 1140  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(1140)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-027-632-117467

Query Match 7.4%; Score 37.2; DB 13; Length 1140;  
Best Local Similarity 49.0%; Pred. No. 21;  
Matches 96; Conservative 1; Mismatches 99; Indels 0; Gaps 0;  
QY 2 TGATTTACAGGAAGACCATGATCTAGCTGCAGCTTCTTAAATCCAGAACGATTTCACGT 61  
Db 616 TGTTTTGTGTTGAATAACATAAAATATTTAAAGTCTCTAATAGTTCATTGTAAGAAAGG 557  
QY 62 CTTATCAGGAAGTAATGAATACATTTCTGGCTGCGAGAGATTTGTTCAATGGTAT 121  
Db 556 CTAATGAGAAATTTGTTAGGACATAGTACACACTGAATGTAGATGCTRT 497  
QY 122 CCATTTGATGAACAGAAATCAATCCATCTGTTTCATGCTTAAGATGTTTGGAAAAAT 181  
Db 496 AAACATAAGCCAGCAAGAACGACATTTATTAGATGTTAGTCTACTTCTCGGAGGAT 437

Query Match 7.4%; Score 37.2; DB 13; Length 1140;  
Best Local Similarity 49.0%; Pred. No. 21;  
Matches 96; Conservative 1; Mismatches 99; Indels 0; Gaps 0;  
QY 2 TGATTTACAGGAAGACCATGATCTAGCTGCAGCTTCTTAAATCCAGAACGATTTCACGT 61  
Db 616 TGTTTTGTGTTGAATAACATAAAATATTTAAAGTCTCTAATAGTTCATTGTAAGAAAGG 557  
QY 62 CTTATCAGGAAGTAATGAATACATTTCTGGCTGCGAGAGATTTGTTCAATGGTAT 121  
Db 556 CTAATGAGAAATTTGTTAGGACATAGTACACACTGAATGTAGATGCTRT 497  
QY 122 CCATTTGATGAACAGAAATCAATCCATCTGTTTCATGCTTAAGATGTTTGGAAAAAT 181  
Db 496 AAACATAAGCCAGCAAGAACGACATTTATTAGATGTTAGTCTACTTCTCGGAGGAT 437  
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US-10-027-632-117466/c  
; Sequence 117466, Application US/10027632  
; Publication No. US20020204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 117466  
LENGTH: 1140  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)...(1140)  
OTHER INFORMATION: n = A,T,C or G  
S-10-027-632-117466

Query Match 7.4%; Score 37.2; DB 16; Length 1140;  
Best Local Similarity 49.0%; Pred. No. 21;  
Matches 96; Conservative 1; Mismatches 99; Indels 0; Gaps 0;  
y 2 TGATTTACAGGAAGACCAGTGTACTAGTCGAGCTTCTAAATCCAGAACGATTTGCAGGT 61  
b 616 TGTGTTTAGTTGAATAACATAAAATATTTAAAGTCTCTAATAGTTTCATTTGAAAAAGAGG 557  
y 62 CTTATCAAGGAGTAATGATACATCTGCGCTGGCAGAGATTTGATTGTTCAATGGTAT 121  
b 556 CTAATGAGAAATGTTGAGAAATTTAGGACATAGTACACACTGAATGTAGATGCTRT 497  
y 122 CCATTTGATGAAACAGAAATCACCACATCTGTTTCATGCTTTAAGATGGTTTGGAAAAAT 181  
b 496 AACATAAGCCAGCAGAGAAAGCACTTATTAGATGGTAGTCTGCTACTTCGGGAGGAT 437  
y 182 CTTTATATACATTTT 197  
b 436 TTTTGTCTCTATATT 421

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ob time : 374.131 secs

GenCore version 5.1.6  
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M nucleic - nucleic search, using sw model

run on: May 26, 2004, 20:25:31 ; Search time 45.0924 Seconds  
(without alignments)  
4935.099 Million cell updates/sec

title: US-09-693-205A-7\_COPY\_5300\_5700  
perfect score: 401  
sequence: 1 gtacagtaaaactaggagc.....actggacagtggaatagg 401

scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

searched: 682709 seqs, 277475446 residues

total number of hits satisfying chosen parameters: 1365418

minimum DB seq length: 0  
maximum DB seq length: 2000000000

post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

database : Issued Patents NA.\*  
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2: /cgn2\_6/prodata/2/ina/5B COMB.seq:\*  
3: /cgn2\_6/prodata/2/ina/6A COMB.seq:\*  
4: /cgn2\_6/prodata/2/ina/6B COMB.seq:\*  
5: /cgn2\_6/prodata/2/ina/PCTUS COMB.seq:\*  
6: /cgn2\_6/prodata/2/ina/backfiles1.seq:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
C 1	42.6	10.6	7218	1	US-08-232-463-14 Sequence 14, Appl
2	34.8	8.7	1607	4	US-08-956-171B-296 Sequence 296, Appl
3	34.2	8.5	981	4	US-09-134-001C-2097 Sequence 2097, Ap
4	33.8	8.4	5385	4	US-09-920-804-1 Sequence 1, Appli
5	33.8	8.4	83450	4	US-09-911-469-3 Sequence 3, Appli
6	33.4	8.3	1365	4	US-09-134-001C-2333 Sequence 2333, Ap
C 7	33.4	8.3	1664976	4	US-08-916-421B-1 Sequence 1, Appli
C 8	33	8.2	1830121	4	US-09-557-884-1 Sequence 1, Appli
C 9	33	8.2	1830121	4	US-09-643-990A-1 Sequence 1, Appli
C 10	32.8	8.2	92407	4	US-09-596-002-36 Sequence 36, Appl
C 11	32.8	8.2	580073	4	US-08-545-528D-1 Sequence 1, Appli
12	32.4	8.1	1335	4	US-09-107-532A-7 Sequence 7, Appli
13	32.4	8.1	1425	4	US-09-134-001C-339 Sequence 339, App
14	32.4	8.1	1651	4	US-09-976-594-598 Sequence 598, App
15	32.2	8.0	4138	4	US-09-920-804-3 Sequence 3, Appli
16	32.2	8.0	5807	4	US-09-976-594-245 Sequence 245, App
C 17	31.8	7.9	350	4	US-09-601-198-137 Sequence 137, App
18	31.8	7.9	1082	4	US-09-641-638-591 Sequence 591, App
19	31.8	7.9	2304	1	US-08-020-245A-7 Sequence 1, Appli
20	31.8	7.9	2304	1	US-08-396-957A-1 Sequence 1, Appli
21	31.4	7.8	2718	4	US-09-717-364A-14 Sequence 14, Appli
22	31.4	7.8	26270	4	US-09-717-364A-1 Sequence 1, Appli
23	31.2	7.8	1332	4	US-09-134-000C-1419 Sequence 1419, Ap
24	31.2	7.8	3030	4	US-09-328-352-4115 Sequence 4115, Ap
25	31.2	7.8	3624	4	US-09-221-017B-398 Sequence 398, App
26	31.2	7.8	4617	4	US-08-930-055A-1 Sequence 1, Appli
27	31.2	7.8	5109	4	US-08-930-055A-2 Sequence 2, Appli

Query Match 10.6%; Score 42.6; DB 1; Length 7218;

ALIGNMENTS

RESULT 1  
US-08-232-463-14/c  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; CLASSIFICATION: 435  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: pTZpT-F15  
; US-08-232-463-14

Sequence 16560, A  
Sequence 30, Appl  
Sequence 4, Appli  
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Sequence 131, App  
Sequence 1, Appli  
Sequence 42, Appl  
Sequence 117, App  
Sequence 216, App  
Sequence 2, Appli  
Sequence 1, Appli  
Sequence 39, Appl  
Sequence 1745, Ap  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 2, Appli  
Sequence 4, Appli

[illegible]

RESULT 2  
 US-08-956-171E-296  
 ; Sequence 296, Application US/08956171E  
 ; Patent No. 6593114  
 ; GENERAL INFORMATION:  
 APPLICANT: Charles Kunsch  
 Gil H. Choi  
 Patrick S. Dillon  
 Craig A. Rosen  
 Steven C. Barash  
 Michael R. Pannon  
 TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
 NUMBER OF SEQUENCES: 5256  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: Maryland  
 COUNTRY: USA  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
 COMPUTER: HP Vectra 486/33  
 OPERATING SYSTEM: MSDOS version 6.2  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/956,171E  
 FILING DATE: 20-Oct-1997  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/009,861  
 FILING DATE: January 5, 1996  
 APPLICATION NUMBER: 08/781,986  
 FILING DATE: January 3, 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mark J. Hyman  
 REGISTRATION NUMBER: 46,789  
 REFERENCE/DOCKET NUMBER: PB248P1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (240) 314-1224  
 TELEFAX: (301) 309-8439  
 INFORMATION FOR SEQ ID NO: 296:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1607 base pairs  
 TYPE: nucleic acid

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RESULT 3
US-09-134-001C-2097
; Sequence 2097, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: LYNN DOUCETTE-STAMM ET AL
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2097
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2097

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RESULT 4  
US-09-920-804-1  
; Sequence 1, Application US/09920804  
; Patent No. 6673899  
; GENERAL INFORMATION:  
; APPLICANT: Seino, Susumu; JCR Pharmaceuticals Co., Ltd.  
; TITLE OF INVENTION: Sodium Ion-driven Chloride/Bi-Carbonate Exchanger  
; FILE REFERENCE: GP44  
; CURRENT APPLICATION NUMBER: US/09/920,804  
; CURRENT FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 8  
; SEQ ID NO 1

LENGTH: 5385  
TYPE: DNA  
ORGANISM: Mus musculus  
S-09-920-804-1

Query Match 8.4%; Score 33.8; DB 4; Length 5385;  
Best Local Similarity 50.3%; Pred. No. 2-2;  
Matches 83; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

33 ACACAAAGCCCTTAGAAGATATGATCCAAATGCTCTTTTACAAACACTTGGCAGCAAGATT 92  
810 ACCAAATTTCCATGATATAAAATGCGAGTCAGGTGTGTTTCTCTCAGTCTGTCTCCAGCCTG 869  
93 TGGCAGAAAGAAAATGACCCAGCAGAAATTAAGACATCCTTAATGCATATCCTTCTGA 152  
870 TGCTGAGAATAAAAATGATGTACGACGGGAAAACAGCACTGTAGACTTCAGCAAGGTTGA 929  
153 AAAGGAAATGTTGAAAGAGCTTCTTCAAAATGCTGATGATGCAAA 197  
930 TCTGCAATTTATGAANAAGATTCTCTCGGGTGTGAAGCTTCAA 974

RESULT 5  
IS-09-811-469-3  
Sequence 3, Application US/09811469  
Patent No. 6551809  
GENERAL INFORMATION:  
APPLICANT: YAN, Chunhua et al.  
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,  
TITLE OF INVENTION: AND USES THEREOF  
FILE REFERENCE: CL001171  
CURRENT APPLICATION NUMBER: US/09/811.469  
CURRENT FILING DATE: 2001-03-20  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 83450  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(83450)  
OTHER INFORMATION: n = A,T,C or G  
IS-09-811-469-3

Query Match 8.4%; Score 33.8; DB 4; Length 83450;  
Best Local Similarity 54.4%; Pred. No. 6.8;  
Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

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145 CTTCTGAAAGAGAAATGTTGAAAGAGCTTCTTCAAAATGCTGATGATGCAAGGCGACA 204  
79231 TCAAAATTAATGTAAATGTTTCCAAACCCCATTAAGAAGAGAGTTAAGTTGGATTCA 79290  
205 GAAAT 209  
79291 AAAGT 79295

RESULT 6  
IS-09-134-001C-2333  
Sequence 2333, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134.001C

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OTHER INFORMATION: n equals a, t, c, or g	t, c, or g
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LOCATION: (98239)..(98239)	t, c, or g
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OTHER INFORMATION: n equals a, t, c, or g	t, c, or g
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LOCATION: (674435)..(674435)	t, c, or g

213 TTTTGTGTTGATCCCTAGACAGCATCCAGTTGATAGATATTTGATGATTAAGTGGGCCCC 272  
 761181 TGGATGATGGACCTATGAGTTTCCAAAGGAGATACTCACTGTTATGGGATTGTTA 761122  
 273 ATTGCAAGGCCAGCACTT 291  
 761121 CTTTAAAGGACCACTTT 761103

RESULT 8  
 US-09-557-884-1/c  
 Sequence 1, Application US/09557884  
 Patent No. 6506581  
 GENERAL INFORMATION:  
 APPLICANT: Fleischmann et al.  
 TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: MD  
 COUNTRY: USA  
 ZIP: 20850

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3 1/2 inch diskette  
 COMPUTER: Dell Pentium  
 OPERATING SYSTEM: MS DOS v6.22  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/557,884  
 FILING DATE: 25-Apr-2000  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/476,102  
 FILING DATE: JUN-5-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Michelle S. Marks  
 REGISTRATION NUMBER: 41,971  
 REFERENCE/DOCKET NUMBER: PB186P3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 301-309-8504  
 TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1830121 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-557-884-1

Query Match 8.2%; Score 33; DB 4; Length 1830121;  
 Best Local Similarity 52.6%; Pred. No. 39;  
 Matches 72; Conservative 0; Mismatches 65; Indels 0; Gaps 0;  
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 1300730 AAGATGTTGTTGTTATTTACATAAAGTTGAGAAAAATTCAGTTAATGCTTGA 1300671  
 226 CCTAGACAGCATCCAGTTGATAGATATTTGATGATTAAGTGGGCCCCATTCGAAGGCCA 285  
 1300670 ACCAAGTGACTGCAGTTGAAGCAAAAGATGATGTTATCTACGTTTCAATGGAAGGCAA 1300611  
 286 GCATTGTTGTGTACAA 302  
 1300610 GCATGTAATGATACCAA 1300594

RESULT 9

US-09-643-990A-1/c  
 Sequence 1, Application US/09643990A  
 Patent No. 6528289  
 GENERAL INFORMATION:  
 APPLICANT: Robert D. Fleischmann  
 Mark D. Adams  
 Owen White  
 Hamilton O. Smith  
 J. Craig Venter  
 TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof  
 NUMBER OF SEQUENCES: 1  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville,  
 STATE: MD  
 COUNTRY: USA  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3 1/2 inch diskette  
 COMPUTER: Dell Pentium  
 OPERATING SYSTEM: MS DOS v6.22  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/643,990A  
 FILING DATE: 23-Aug-2000  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/487,429  
 FILING DATE: 1995-06-07  
 APPLICATION NUMBER: 08/426,787  
 FILING DATE: 1995-04-21  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kenley K. Hoover  
 REGISTRATION NUMBER: 40,302  
 REFERENCE/DOCKET NUMBER: PB186PIC1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 301-610-5790  
 TELEFAX: 310-309-8439  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1830121 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-643-990A-1

Query Match 8.2%; Score 33; DB 4; Length 1830121;  
 Best Local Similarity 52.6%; Pred. No. 39;  
 Matches 72; Conservative 0; Mismatches 65; Indels 0; Gaps 0;  
 166 AAGAGCTTCTTCAAAATGCTGATGCAAGGCGACAGAAATCTGTTTGTGTTGAT 225  
 1300730 AAGATGTTGTTGTTATTTACATAAAGTTGAGAAAAATTCAGTTAATGCTTGA 1300671  
 226 CCTAGACAGCATCCAGTTGATAGATATTTGATGATTAAGTGGGCCCCATTCGAAGGCCA 285  
 1300670 ACCAAGTGACTGCAGTTGAAGCAAAAGATGATGTTATCTACGTTTCAATGGAAGGCAA 1300611  
 286 GCATTGTTGTGTACAA 302  
 1300610 GCATGTAATGATACCAA 1300594

RESULT 10  
 US-09-596-002-36  
 Sequence 36, Application US/09596002  
 Patent No. 6632636  
 GENERAL INFORMATION:  
 APPLICANT: Lagace, Robert, E.



APPLICANT: Patterson, Chandra  
APPLICANT: Berg, Kim, L.  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME  
FILE REFERENCE: PM-0008-4 US  
CURRENT APPLICATION NUMBER: US/09/596,002  
CURRENT FILING DATE: 2000-06-16  
PRIOR APPLICATION NUMBER: 60/140,121  
PRIOR FILING DATE: 1999-06-18  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PERL Program  
SEQ ID NO 36  
TYPE: DNA  
LENGTH: 92407  
ORGANISM: M. catarrhalis  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte template ID No. 6632636 36  
PUBLICATION INFORMATION:  
US-09-596-002-36

Query Match 8.2%; Score 32.8; DB 4; Length 92407;  
Best Local Similarity 50.0%; Pred. No. 14;  
Matches 82; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 130 ATCCCTTAATGCATATCCTTCTGAAAGGAAATGTTGAAAGAGCTTCTTCAAAATGCTCAT 189  
DB 70322 ATTACTAGTCAATGATTTTAAATAATTTGGTCTACTAGTCCTTTAAATATTAA 70381

QY 190 GATGCAAGGCGACAGAAATCTGTTTGTGTTGATCCTGACAGCATCCAGTTGATAGA 249  
DB 70382 ATTGTAAGGCGACCCCAATGCTTTCTTTTAAAGGACCCATAGCAAGTTGCAGATT 70441

QY 250 ATATTTGATGAAGGCGCCCATTCGACGGCCGACGACATTG 293  
DB 70442 CTTTTTCTTACATGATCTTAATTTATCGCCTTGATCTG 70485

RESULT 11  
US-08-545-528D-1/c  
Sequence 1, Application US/08545528D  
Patent No. 6537773  
GENERAL INFORMATION:  
APPLICANT: Fraser et al.  
TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment  
FILE REFERENCE: P8193P1  
CURRENT APPLICATION NUMBER: US/08/545,528D  
CURRENT FILING DATE: 1995-10-19  
PRIOR APPLICATION NUMBER: US 08/488,018  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: US 08/473,545  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 1  
LENGTH: 580073  
TYPE: DNA  
ORGANISM: Mycoplasma genitalium  
US-08-545-528D-1

Query Match 8.2%; Score 32.8; DB 4; Length 580073;  
Best Local Similarity 48.0%; Pred. No. 30;  
Matches 94; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 73 ACAACACTTGGCAGCAATTTGGCGAGAAAGAAATTCACCGAGCAATTAAGAGCATC 132  
DB 412879 AAAACACTTTTAAAGAAATTAGTACAAAGAACTTAATAATATCCTTTTCCACATCTAAA 412820

QY 133 CTTAATGCATATCCTTCTGAAAGGAAATGTTGAAGAGCTTCTTCAAAATGCTCATGAT 192  
DB 412819 ATTACTGCTATCCCTTTGAAAGAAATTTATTGGAGAAACATTTTGGTACTGTTGAT 412760

QY 193 GCAAGGCGACAGAAATCTGTTTGTGTTGATCCTAGACAGCATCCAGTTGATAGAATA 252  
DB 412759 GAAGCTGAGAAGAAAGTCAATAGTTCTTTTTTAATGGAATAGATTAAGGTT 412700

QY 253 TTTGATGATAAGTGGG 268  
DB 412699 TTAGATAAAATGGG 412684

RESULT 12  
US-09-107-532A-7  
Sequence 7, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1335 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...1335  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-107-532A-7

Query Match 8.1%; Score 32.4; DB 4; Length 1335;  
Best Local Similarity 52.2%; Pred. No. 3.2;  
Matches 72; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 128 GCATCCTTAATGCATATCCTTCTGAAAGGAAATGTTGAAGAGCTTCTTCAAAATGCTG 187  
DB 473 GTATCGTATTGCAGACTTATTAGATAAAGAAATTTTGAAGACGTTCTTCTTGAATC 532

QY 188 ATGATCCAAAGCGCAGAAAATCTGTTTGTGTTTGTATCCTAGACAGCATCCAGTTGATA 247  
DB 533 TAGATGACAAAACCGTCAATTTGTAATAAATGTTGATTCAAGACCACTTGATTTTGACG 592

248 GAATATTTGATGATAGT 265  
593 ATATTTTGAAGAATAT 610

Sequence 339, Application US/09134001C  
Patent No. 6380370

GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GPC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 339  
LENGTH: 1425  
TYPE: DNA  
ORGANISM: Staphylococcus epidermidis

JS-09-134-001C-339

Query Match 8.1%; Score 32.4; DB 4; Length 1425;  
Best Local Similarity 46.8%; Pred. No. 3.3; Indels 0; Gaps 0;  
Matches 102; Conservative 0; Mismatches 116

46 GAAAGATATGATCCCAATGCTGTTTACAACTTGGCAGAGAAATTTGGGCGAGAAAGAA 105  
49 GCAGATATGATGCGCCATCAGAGCTTCTCAATTAGGAAAAAGTAGCGATAGTAA 108  
106 AAATGACGAGCAGAAATTAAGAGCACTTAAATGATATCTCTCTGAAAGGAATGTTG 165  
109 AAATCACTCTTAGTGTGCTGTTTACATAAAGGATGATACCTACTAAAGCACTTTTA 168  
166 AAAGAGCTTCTCAAAATGCTGATGATGCAAAAGCGCAGAGAAATCTGTTTGTGTTGAT 225  
169 AAATCGCTGAGTCAATCATATTAATAAAGCGCATACATTTGGAAATGATGTCAT 228  
226 CCTAGACAGATCAGTTGATAGAAATTTGATGATAA 263  
229 CATTTTAAATTAATTTCCCTAAATTTTAGAACGTAA 266

Sequence 598, Application US/09976594  
Patent No. 6673549

GENERAL INFORMATION:  
APPLICANT: Furness, Michael  
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS  
FILE REFERENCE: PA-0041 US  
CURRENT APPLICATION NUMBER: US/09/976,594  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 60/240,409  
PRIOR FILING DATE: 2000-10-12  
NUMBER OF SEQ ID NOS: 1143  
SOFTWARE: PERL Program  
SEQ ID NO 598  
LENGTH: 1651  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. 6673549 344186.12

JS-09-976-594-598

Query Match 8.1%; Score 32.4; DB 4; Length 1651;  
Best Local Similarity 60.0%; Pred. No. 3.5; Indels 0; Gaps 0;  
Matches 54; Conservative 0; Mismatches 36

15 AGAGCAGTCCCAAGCGACACAAAGCCTTAGAAGATATGATCCATGCTGTTTAC 74  
827 AGAGCTTCTACAGCGCAAAAGAAAGTCTGGAAGTCAATGGATCGCAGAAATCTTTG 886  
75 AACACTTGGCAGAGAAATTTGGGCGAGAAAGA 104  
887 AAAAATTTGCAGAAATGTTGGCGAGAAACA 916

Sequence 3, Application US/09920804  
Patent No. 6673899

GENERAL INFORMATION:  
APPLICANT: Seino, Susumu; JCR Pharmaceuticals Co., Ltd.  
TITLE OF INVENTION: Sodium Ion-Driven Chloride/Bi-Carbonate Exchanger  
FILE REFERENCE: GP44  
CURRENT APPLICATION NUMBER: US/09/920,804  
CURRENT FILING DATE: 2001-08-03  
NUMBER OF SEQ ID NOS: 8  
SEQ ID NO 3  
LENGTH: 4138  
TYPE: DNA  
ORGANISM: Homo sapiens

US-09-920-804-3

Query Match 8.0%; Score 32.2; DB 4; Length 4138;  
Best Local Similarity 49.7%; Pred. No. 5.9; Indels 0; Gaps 0;  
Matches 82; Conservative 0; Mismatches 83

33 ACACAAAGCCTTAGAAGATATGCAATCTGTTTACAACTTGGCAGAGAAAT 92  
826 ACCAAATTCATGCGACAAAATGCAGTCAAGTTGTTCTCTCAGTCTGCTCCAGCTG 885  
93 TGGGCGAAGAAATAATGCAGCGAGAAATTAAGAGCATCTTAATGATATCTCTTGA 152  
886 TGTTGAAAATAAAATGATGTTAGCAGAGAAACAGCACTGTTGACTTTAGCAAGTTGA 945  
153 AAAGGAAATGTTCAAGAGCTTCTTCAAAATGCTGATGATGCAA 197  
946 TCTGCAATTTATGAAAAGAAATTCCTCCAGTCTGAAGCATCGAA 990

Search completed: May 26, 2004, 22:17:47  
Job time : 54.0924 secs

## SUMMARIES

result No.	Score	Query #		Length	DB	ID	Description
		Match					
1	401	100.0	11490	13	US-10-342-887-1480	Sequence 1480, Ap	
2	401	100.0	11490	13	US-10-172-118-1480	Sequence 1480, Ap	
3	39.8	9.9	405	13	US-10-424-599-107847	Sequence 107847,	
4	39	9.7	853	13	US-10-027-633-174049	Sequence 174049,	
5	39	9.7	853	16	US-10-027-633-174049	Sequence 174049,	
6	36.6	9.1	954	13	US-10-282-122A-16079	Sequence 16079, A	
7	36.2	9.0	1116	13	US-10-282-122A-18335	Sequence 18335, A	
8	35.8	8.9	54945	10	US-09-367-669-10	Sequence 10, Appl	
9	34.8	8.7	857	16	US-10-369-493-30535	Sequence 30535, A	
10	34.8	8.7	1281	9	US-03-815-242-4620	Sequence 4620, Ap	
11	34.8	8.7	1284	8	US-03-815-442-8577	Sequence 8577, Ap	
12	34.8	8.7	1607	8	US-03-781-986A-296	Sequence 296, App	
13	34.8	8.7	1607	13	US-10-329-624-296	Sequence 296, App	
14	34.8	8.7	3825	13	US-10-282-122A-17088	Sequence 17088, A	

Dbb 5224 GTAGCAGTAAACTAGGAGCAGTCCCC

b  
5224 GTAGCAGTAAACTAGGAGCAGTCCCAAGCGACACAAAG

QY 61 AATGCTCTGTTTACAACTTGGCCACAGAAATTTGGGCGAAGAAATTTGACCCAGCAGA 120  
Db 5284 AATGCTCTGTTTACAACTTGGCCACAGAAATTTGGGCGAAGAAATTTGACCCAGCAGA 5343  
QY 121 ATTAAGAGCATCCTTAAATGCATATCCTTTCTGAAAAGGAAATGTTTGAAGAGCTTCTTCAA 180  
Db 5344 ATTAAGAGCATCCTTAAATGCATATCCTTTCTGAAAAGGAAATGTTTGAAGAGCTTCTTCAA 5403  
QY 181 AATGCTGATGATGCAAGGCGACAGAAATCTGTTTGTGTTTGTATCTAGACAGCATCCA 240  
Db 5404 AATGCTGATGATGCAAGGCGACAGAAATCTGTTTGTGTTTGTATCTAGACAGCATCCA 5463  
QY 241 GTTGATAGAAATTTGATGATAAGTGGGCCCATTTGCAAGGGCCAGCACATTTTGTGTGATC 300  
Db 5464 GTTGATAGAAATTTGATGATAAGTGGGCCCATTTGCAAGGGCCAGCACATTTTGTGTGATC 5523  
QY 301 AACACCCAGCCATTTACAGAGATGATGTTAGAGAAATTCAGAAATCTTGAAGAGGACG 360  
Db 5524 AACACCCAGCCATTTACAGAGATGATGTTAGAGAAATTCAGAAATCTTGAAGAGGACG 5583  
QY 361 AAAGAGGAAATCCTTATATAAACTGGACAGTATGGAATAGG 401  
Db 5584 AAAGAGGAAATCCTTATATAAACTGGACAGTATGGAATAGG 5624  
RESULT 2  
US-10-172-118-1480  
; Sequence 1480, Application US/10172118  
; Publication No. US20030224374A1  
; GENERAL INFORMATION:  
; APPLICANT: Dai, Hongyue  
; APPLICANT: He, Yudong  
; APPLICANT: Linsley, Peter  
; APPLICANT: Mao, Mao  
; APPLICANT: Roberts, Chris  
; APPLICANT: Van't Veer, Laura  
; APPLICANT: Van de Vijver, Marc  
; APPLICANT: Bernards, Rene  
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
; FILE REFERENCE: 9301-175-999  
; CURRENT APPLICATION NUMBER: US/10/172,118  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: 60/380,770  
; PRIOR FILING DATE: 2002-05-14  
; NUMBER OF SEQ ID NOS: 2699  
; SEQ ID NO 1480  
; LENGTH: 11490  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: NM\_014363  
; DATABASE ENTRY DATE: 2001-06-18  
US-10-172-118-1480  
Query Match 100.0%; Score 401; DB 13; Length 11490;  
Best Local Similarity 100.0%; Pred. No. 5,5e-104;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTAGCAGTAAATAGGACAGTCCCAAGCGACACAAAGCCTTAGAAAGATATGCATCC 60  
Db 5224 GTAGCAGTAAATAGGACAGTCCCAAGCGACACAAAGCCTTAGAAAGATATGCATCC 5283  
QY 61 AATGCTGTTTACACACTTGGCCACAGAAATTTGGGCGAAGAAATTTGACCCAGCAGA 120  
Db 5284 AATGCTGTTTACACACTTGGCCACAGAAATTTGGGCGAAGAAATTTGACCCAGCAGA 5343  
QY 121 ATTAAGAGCATCCTTAAATGCATATCCTTTCTGAAAAGGAAATGTTTGAAGAGCTTCTTCAA 180  
Db 5344 ATTAAGAGCATCCTTAAATGCATATCCTTTCTGAAAAGGAAATGTTTGAAGAGCTTCTTCAA 5403  
QY 181 AATGCTGATGATGCAAGGCGACAGAAATCTGTTTGTGTTTGTATCTAGACAGCATCCA 240

Db 5404 AATGCTGATGATGCAAGGCGACAGAAATCTGTTTGTGTTTGTATCTAGACAGCATCCA 5463  
QY 241 GTTGATAGAAATTTGATGATAAGTGGGCCCATTTGCAAGGGCCAGCACATTTTGTGTGATC 300  
Db 5464 GTTGATAGAAATTTGATGATAAGTGGGCCCATTTGCAAGGGCCAGCACATTTTGTGTGATC 5523  
QY 301 AACACCCAGCCATTTACAGAGATGATGTTAGAGAAATTCAGAAATCTTGAAGAGGACG 360  
Db 5524 AACACCCAGCCATTTACAGAGATGATGTTAGAGAAATTCAGAAATCTTGAAGAGGACG 5583  
QY 361 AAAGAGGAAATCCTTATATAAACTGGACAGTATGGAATAGG 401  
Db 5584 AAAGAGGAAATCCTTATATAAACTGGACAGTATGGAATAGG 5624  
RESULT 3  
US-10-424-599-107847  
; Sequence 107847, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 107847  
; LENGTH: 405  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_68401C.1  
US-10-424-599-107847  
Query Match 9.9%; Score 39.8; DB 13; Length 405;  
Best Local Similarity 47.7%; Pred. No. 0.42; 127; Indels 0; Gaps 0;  
Matches 116; Conservative 0; Mismatches 127; Indels 0; Gaps 0;  
QY 87 AGAATTTGGGCGAAGAAATTTGACCCAGCAGAAATTAAGAGCATTCCTTAATGCATATCC 146  
Db 148 AGACITTCGGCCAGACGGTTGATCTGACGCGCGCATCCGGAGGTTCTGCTCAACTACCC 207  
QY 147 TTCTGAAAAGGAAATGTTGAAGAGCTTCTTCAAATGCTGATGATCAAAGGCGCAGA 206  
Db 208 GGAGGAAACCCCGTCTCTGAAGAGGCTCTATACAGACGCGCAGCCGCCGCCAC 267  
QY 207 AATCTGTTTGTGTTTGTATCTTAGACAGCATCCAGTTGATAGATATTTGATGATAAGTG 266  
Db 268 CGTCTCTCTGCTCGACCGCTCCACCTCGCGGCTCCCTGCTCTCCGACTCCCT 327  
QY 267 GCGCCCATTTGCAAGGCGCCAGCACATTTGTTGTGTACAAACAGCCATTTACAGAGATGA 326  
Db 328 CGCGCAGTGGCGGAGGACCGCAGCTGTTGCTTCAACGACGCGCTCTTCCCGGAGGA 387  
QY 327 TGT 329  
Db 388 TTT 390  
RESULT 4  
US-10-027-632-174049  
; Sequence 174049, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632

Query Match 9.7%; Score 39; DB 16; Length 853;  
Best Local Similarity 56.7%; Pred. No. 1;  
Matches 72; Conservative 0; Mismatches 55; Indels 0; Gaps 0;  
  
QY 37 AAAGCCTTAGAAGATATGCAATCTCTGTTTACAACTTGGCAGAGAAATTTGGG 96  
DB 16 AAATTCACAGAACTGTATGCTTACAAATTTGAACTTACTAGATAGAACTCAATAAATGA 75  
  
QY 97 CAGAAAGAAAATTCACAGCAGAGAAATTAAGAGCATCCCTTAATGCATATCCTTCTGAAAAG 156  
DB 76 CAGAAACAAAATAACAGAAAATAAAGCTTGGTTTCTGATCTTCTAAGCATAATG 135  
  
QY 157 GAAATGT 163  
DB 136 GAACTGT 142

RESULT 6  
US-10-282-122A-16079  
; Sequence 16079, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITEA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16079  
; LENGTH: 954  
; TYPE: DNA  
; ORGANISM: Clostridium botulinum  
US-10-282-122A-16079

Query Match 9.1%; Score 36.6; DB 13; Length 954;  
Best Local Similarity 47.9%; Pred. No. 5.3;  
Matches 105; Conservative 0; Mismatches 114; Indels 0; Gaps 0;  
  
QY 73 ACACACTTGGCAGAAATTTGGGCGAGAAAGAAATTCACCAGAGAAATTAAGAGCATC 132

CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 174049  
LENGTH: 853  
TYPE: DNA  
ORGANISM: Human  
S-10-027-632-174049  
  
Query Match 9.7%; Score 39; DB 13; Length 853;  
Best Local Similarity 56.7%; Pred. No. 1;  
Matches 72; Conservative 0; Mismatches 55; Indels 0; Gaps 0;  
  
Y 37 AAAGCCTTAGAAGATATGCAATCTCTGTTTACAACTTGGCAGAGAAATTTGGG 96  
b 16 AAATTCACAGAACTGTATGCTTACAAATTTGAACTTACTAGATAGAACTCAATAAATGA 75  
  
Y 97 CAGAAAGAAAATTCACAGCAGAGAAATTAAGAGCATCCCTTAATGCATATCCTTCTGAAAAG 156  
b 76 CAGAAACAAAATAACAGAAAATAAAGCTTGGTTTCTGATCTTCTAAGCATAATG 135  
  
Y 157 GAAATGT 163  
b 136 GAACTGT 142

RESULT 5  
S-10-027-632-174049  
Sequence 174049, Application US/10027632  
Publication No. US20030204075A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 174049  
LENGTH: 853  
TYPE: DNA  
ORGANISM: Human  
S-10-027-632-174049

502 AGAAAAATTTTTCACAGAGATGCACTACCCCTAAATATGATGACAAATTTGAACTATA 561

133 CTTAATGCATATCCTTCTGAAAAGAAATGTTGAAGAGCTTCTTCAAAATGCTGATGAT 192

562 AAAAATGCAGAAAGAAAGCTGGTATTGAGATATGTATGCTGGAAATATATGCTCTTGGAGAA 621

193 GCAAGGCGCAGAGAAATCTGTTTTGTGTTTGATCCTACAGACGATCCAGTTGTATAGATA 252

622 ACCATGGAGGACCGAATCGATATGCTTTTACTTTTAAGAGAGCTTTTCAGTTGAAAGTGTT 681

253 TTTTGATGATAGTGGGGCCCCATTGCAAGGGCCAGCACTT 291

682 CCAGTTAATATCTTTAACTCTATTAAAGGAACCACTT 720

## RESULT 7

US-10-282-122A-18335  
Sequence 18335, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haseibeck, Robert  
APPLICANT: Ohlsen, Karl  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.

	Query Match	9.0%;	Score 36.2;	DB 13;	Length 1116;
	Best Local Similarity	48.8%;	Pred. No. 7.5;		
	Matches 98;	Conservative	0;	Mismatches 103;	Indels 0;
	Gaps	0			
QY	63	TGTCGTTTTTCAACACTGGCACAGAAATTTGGCGCAAGAAAAATTCACACGACGAAAT	122		
DB	867	TTTATATCTTAATATAATGGAAATTTTAGTTGGTTCAAGGCAAGATGGTGAACATGACAT	926		

Qy	123	TAAGAGCATCCTTAAATGCATATCCTTCTGAAAGGAAATGTTGAAGAGCGCTTCTTCAAAA	182
Db	927	TAATAAAACCAATAGAGTAAATGCAGAGAAAGGATATATGGAGCGATTTTAAATAC	986
Qy	183	TCGCTGATGATGCAAGGCGACAGAAATCTGTTTGTGTTGATCCTAGACAGATCCAGT	242
Db	987	TAGTAAATGCACTAATATACAAATAAAGACTAGAAAAATTTAAATAGTTCTTGAGCAATT	1046
Qy	243	TGATAGATAATTTGATGATAA	263
Db	1047	TTATAGGTTATTGAAAAATAA	1067

## RESULT 8

```

US-09-967-669-10
; Sequence 10, Application US/09967669
; Publication No. US20030092650A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION
; FILE REFERENCE: RTS-0259
; CURRENT APPLICATION NUMBER: US/09/967,669
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 10
; LENGTH: 54945
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-669-10

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Query Match	8.9%	Score 35.8	DB 10	Length 54945
Best Local Similarity	52.3%	Pred. No. 73		
Matches 102	Conservative 0	Mismatches 92	Indels 1	Gaps 1
QY	30	GCACACAAAGCCTTTGAAGATATGCATCCCAATCTCTGTTTTCACACACTTGGCACAGA	89	
Db	2711	GCACAGCCAGACTTTGAAGAGATGAGAACTGGTTAGAACTTTCGACTCTTATCCGGGA	2770	
QY	90	ATTTGGGCAGAAAGAAAATTGACACAGCAGAAATTAAGAGCATCTTAAATGCATATCTTC	149	
Db	2771	ATGTACAAAATACAGATGACTGGGGCTCACCTCATTCCTCCATCTGCAGAGAGGCC	2830	
QY	150	TGAAAAGGAAATGTTGAAAGAGCTTCTTCAAAATCTGATGATCCAAAGCGCAGACAAT	209	
Db	2831	TGACATGTGGATTTGAAAG-GCTCCTTGGAGATCTGACTATCCATCTAGATGGGCAC	2889	
QY	210	CTGTTTGTGTTTGA	224	
Db	2890	CTGGATGATGTTTAA	2904	

## RESULT. T 9

```

US-10-369-493-30535
; Sequence 30535, Application US/10369493
; Publication NO. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 30535
; LENGTH: 857
; TYPE: DNA

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ORGANISM: *Caenorhabditis elegans*  
10-369-493-30535

Query Match	8.7%;	Score 34.8;	DB 16;	Length 857;
Best Local Similarity	50.6%;	Pred. No. 17;		
Matches 84;	Conservative 0;	Mismatches 82;	Indels 0;	Gaps 0;
2	TAGCAGTAAACCTAGGAGCAGTCCCAAAGCCACACAAGCCTTTAGAAAGATATGCATCCA	61		
339	TAAACAAATATGTTAGTTAACTGGCCACCCCAAAAAGATGAATTTCAAGCTTTTAATCAT	398		
62	ATGCTCTGTTTTCACACACTGTGCACAGAAATTTGGCAGAAAGAAAATTTGCACACAGAA	121		
399	ATTATATTTTCTCCAAAATGAGGAAAAATGCTGTAATAGAGAACAATAATTTTCAACGTAA	458		
122	TTAAGAGCATCCCTTAATGCAATATCCTTCTGAAAAGGAAATGTTGAA	167		
459	CTATGATCTTTCTTGATATCTTTCTGTTATCGGCGAAACTATAAA	504		

```

RESULT 10
3-09-815-242-4620
Sequence 4620, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlseen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4620
LENGTH: 1281
TYPE: DNA
ORGANISM: Staphylococcus aureus
3-09-815-242-4620

```

	Query Match	8.7%;	Score 34.8;	DB 9;	Length 1281;
	Best Local Similarity	47.3%;	Prod. No. 20;		
	Matches 105;	Conservative	0;	Mismatches 117;	Indels 0; Gaps 0;
y	123	TAAGAGCATCCTTAATGCAATATCCCTCTCGAAAGGAAATGTTGAAGAGGCTTCTTCAAA	182		
b	426	TATCGGTATTCGTATGGCGAGTTTACTTGAATAAGAAACATTCGAAAGATTATTAAATC	485		
y	183	TGCTGATGATGCAAGGCGACAGAAATCGTTTTCGTTTTCATCTCAGACAGCATCCAGT	242		
b	486	AAACATGTAATATAAACAAGCATATTTCAAGGTATGTTTAAACGAAACATGTCCATCAT	545		
y	243	TGATAGAAATTTTGATGATATAAGTGGGCCCCCATTCGAAGGGCCAGCATTTTGTGTGTA	302		

Db	546	TCATGATATCTTTGAAGAAATTATGACGAGGTCAACGCTTAAGAAGATTTGTTAACAGA	605
Qy	303	CAACCGCCATTACAGACATGATGTTAGAGGAATTCAGAA	344
Db	606	CACATCAAAATCTTACAGCATGATTTGTAGCAGATGAAA	647

```

RESULT 11
US-09-815-242-8577
Sequence 8577, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011a
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8577
LENGTH: 1284
TYPE: DNA
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1284)
US-09-815-242-8577

```

	Query Match	8.7%;	Score 34.8;	DB 9;	Length 1284;
	Best Local Similarity	47.3%;	Pred. No. 20;		
	Matches 105;	Conservative 0;	Mismatches 117;	Indels 0;	Gaps 0;
Qy	123	TAAGAGCATCTTAAATGCATATCCTCTCGAAAAGGAATGTTGAAAGAGCTTCTTCAAAA	182		
Db	426	TATCGGTATTGTTATGCGAGNTTACTTTGAAAAGAAACATTCGAAAGATTATTAAATC	485		
Qy	183	TGCTGATGATGCAAGGGCGACAGAAATCTGTTTTGTGTTTGATCTCTAGACGATCCAGT	242		
Db	486	AAACATTGAATATAAAACAAGCATATTTCAAAGGTATGTTTTAAACGAAACATGTGCCATCAIT	545		
Qy	243	TGATAGATATTTTGATGATAGTGGGCCCATTTGCAAGGCCGACATTTGTGTGTACAA	302		
Db	546	TGATGATATCTTTGAAGAATATTATGCGCGAGGTCAACGTCTTAAGAAATTTGTTAACAGA	605		
Qy	303	CAACAGGCCATTTACAGAAAGATGATGTTAGAGGAATTCAGAA	344		
Db	606	CACATCAAAATCTTTAGACCATGATGATTTGTAGCAGATGAAA	647		

## RESULT 12

US-08-781-986A-296  
; Sequence 296, Application US/08781986A  
; Publication No. US20030054436A1  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunech  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5255  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/781,986A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Benson, Bob  
; REGISTRATION NUMBER: 30,446  
; REFERENCE/DOCKET NUMBER: PB248PP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 296:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1607 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; US-08-781-986A-296  
Query Match 8.7%; Score 34.8; DB 8; Length 1607;  
Best Local Similarity 47.3%; Pred. No. 23;  
Matches 105; Conservative 0; Mismatches 117; Indels 0; Gaps 0;  
QY 123 TAAGAGCATCTTAATGCATATCCTTCTGAAAGGAATGTTGAAGAGCTTCTTCAAAA 182  
Db 548 TATCGGTATTCGTATGCGAGATTTACTTGAAGAAGAAACATTCGAAGATTATTAAATC 607  
QY 183 TGCTGATGATGCAAGGCGACAGAAATCTGTTTGTGTTTGTATCCTTAGACAGCATCCAGT 242  
Db 608 AAACATTGAATATAAACAAGCATATTTCAAAGGTATGTTTAAAGAAACATGTCATCAT 667  
QY 243 TGATAGATATTTGATGATAGTAAAGTGGCCCATTTGCGAGGCCAGCATTTGTGTGTACAA 302  
Db 668 TGATGATATCTTTGAAGATATTATGACAGCATCAACGTTCTAAAGAAATTTGTAAACAGA 727  
QY 303 CAACAGCGCATTTACAGAAGATGATGTTAGAGGAATTCAGAA 344  
Db 728 CACATCAAAAATCTTAGACGATGATTTGTAGCAGATGAAA 769

RESULT 13  
US-10-329-624-296  
; Sequence 296, Application US/10329624  
; Publication No. US20040043037A1  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunech  
; Gil H. Choi  
; Patrick S. Dillon  
; Craig A. Rosen  
; Steven C. Barash  
; Michael R. Fannon

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5256  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/329,624  
; FILING DATE: 27-Dec-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/956,171  
; FILING DATE: October 20, 1997  
; APPLICATION NUMBER: 60/009,861  
; FILING DATE: January 5, 1996  
; APPLICATION NUMBER: 08/781,986  
; FILING DATE: January 3, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mark J. Hyman  
; REGISTRATION NUMBER: 46,789  
; REFERENCE/DOCKET NUMBER: PB249P1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (240) 314-1224  
; TELEFAX: (301) 309-8439  
; INFORMATION FOR SEQ ID NO: 296:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1607 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 296:  
; US-10-329-624-296  
Query Match 8.7%; Score 34.8; DB 13; Length 1607;  
Best Local Similarity 47.3%; Pred. No. 23;  
Matches 105; Conservative 0; Mismatches 117; Indels 0; Gaps 0;  
QY 123 TAAGAGCATCTTAATGCATATCCTTCTGAAAGGAATGTTGAAGAGCTTCTTCAAAA 182  
Db 548 TATCGGTATTCGTATGCGAGATTTACTTGAAGAAGAAACATTCGAAGATTATTAAATC 607  
QY 183 TGCTGATGATGCAAGGCGACAGAAATCTGTTTGTGTTTGTATCCTTAGACAGCATCCAGT 242  
Db 608 AAACATTGAATATAAACAAGCATATTTCAAAGGTATGTTTAAAGAAACATGTCATCAT 667  
QY 243 TGATAGATATTTGATGATAGTAAAGTGGCCCATTTGCGAGGCCAGCATTTGTGTGTACAA 302  
Db 668 TGATGATATCTTTGAAGATATTATGACAGCATCAACGTTCTAAAGAAATTTGTAAACAGA 727  
QY 303 CAACAGCGCATTTACAGAAGATGATGTTAGAGGAATTCAGAA 344  
Db 728 CACATCAAAAATCTTAGACGATGATTTGTAGCAGATGAAA 769

RESULT 14  
US-10-282-122A-17088  
; Sequence 17088, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel



APPLICANT: Trawick, John  
 APPLICANT: Garz, Grant  
 APPLICANT: Yamamoto, Robert  
 APPLICANT: Forsyth, R.  
 APPLICANT: Xu, H.  
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 FILE REFERENCE: ELITRA.034A  
 CURRENT APPLICATION NUMBER: US/10/282,122A  
 CURRENT FILING DATE: 2003-02-20  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: 60/191,078  
 PRIOR APPLICATION NUMBER: 60/206,848  
 PRIOR FILING DATE: 2000-05-23  
 PRIOR APPLICATION NUMBER: 60/207,727  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: 60/230,335  
 PRIOR FILING DATE: 2000-09-06  
 PRIOR APPLICATION NUMBER: 60/230,347  
 PRIOR FILING DATE: 2000-09-09  
 PRIOR APPLICATION NUMBER: 60/242,578  
 PRIOR FILING DATE: 2000-10-23  
 PRIOR APPLICATION NUMBER: 60/253,625  
 PRIOR FILING DATE: 2000-11-27  
 PRIOR APPLICATION NUMBER: 60/257,931  
 PRIOR FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: 60/267,636  
 PRIOR FILING DATE: 2001-02-09  
 PRIOR APPLICATION NUMBER: 60/269,308  
 PRIOR FILING DATE: 2001-02-16  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 78614  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 17088  
 LENGTH: 3825  
 TYPE: DNA  
 ORGANISM: Clostridium difficile  
 JS-10-282-122A-17088  
  
 Query Match 8.7%; Score 34.8; DB 13; Length 3825;  
 Best Local Similarity 45.8%; Pred. No. 36;  
 Matches 120; Conservative 0; Mismatches 142; Indels 0; Gaps 0;  
  
 2Y 2 TAGCAGTAAACTAGGACGACCTCCCAAGGACACCAAGCCTTAGAAGATATGCATCCA 61  
 3407 TAACAGAAAAACAGCTAGTATAGTAAATCCATATAAATAATATAAATTTTGGCTCTA 3466  
  
 2Y 62 ATGCTGTGTTTACACACTTGGCCACAGAAATTTGGCCAGAAAGAAATTTGACCCAGAA 121  
 3467 ACATAGGAAAAAGAAATGTTGAATCTGAATTTAATATAGAGAAATCCATTTATGCAC 3526  
  
 2Y 122 TTAAGAGCATCCTTAATGCATCTCTCGAAGGAAATGTTGAAGAGCTTCTTCAA 181  
 3527 AAGTAAATATGAAGACATATATATTTATGAAGCTTATAAACAATGATGATAAAAAAC 3586  
  
 2Y 182 ATGCTGATGATGCAAGGCGACAGAAATCTGTTTGTGTTTGTATCCTAGACAGATCCAG 241  
 3587 TTTATGATAATGAAAGTCTCATGTTGAAGGTATAGTTGATGCTTATTTTGAAGAAGATA 3646  
  
 2Y 242 TTGATAGATATTTGATGATGATA 263  
 DB 3647 ATCAAAATAGTTTGTGTTGATTA 3668  
  
 RESULT 15  
 US-10-311-455-1702  
 ; Sequence 1702, Application US/10311455  
 ; Publication No. US20030143606A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OLEK, Alexander  
 ; APPLICANT: PIEPENEROCK, Christian  
 ; APPLICANT: BERLIN, Kurt  
 ; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation  
 ; FILE REFERENCE: 5013.1014  
 ; CURRENT APPLICATION NUMBER: US/10/311,455  
 ; CURRENT FILING DATE: 2002-12-16  
 ; PRIOR FILING DATE: PCT/EP01/07537  
 ; PRIOR FILING DATE: 2001-07-02  
 ; PRIOR APPLICATION NUMBER: DE 10032529.7  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: DE 10043826.1  
 ; PRIOR FILING DATE: 2000-09-01  
 ; NUMBER OF SEQ ID NOS: 2424  
 ; SEQ ID NO 1702  
 ; LENGTH: 17721  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
 US-10-311-455-1702  
  
 Query Match 8.7%; Score 34.8; DB 15; Length 17721;  
 Best Local Similarity 51.3%; Pred. No. 79;  
 Matches 81; Conservative 0; Mismatches 77; Indels 0; Gaps 0;  
  
 QY 95 GGCAGAAAGAAAAATGACGACAGATTAAGAGCATCTTTAATGCATATCCTTCTGAAA 154  
 DB 8323 GGATGAAATTTAAATAGTTATGATAAATAAAGAAACGTGATAAAAAAGGTATTTATT 8382  
  
 QY 155 AGCAATGTTGAAGAGCTTCTTCAAAATGCTGATGCGAAAGCGACAGAAATCTGTT 214  
 DB 8383 ATTTTACGTTTATAAAAAATTTTAAAAATGTAGGTTAATTTATGCGTATAGAAAAGTAGAT 8442  
  
 QY 215 TTGCTGTTGATCCTAGACAGCATCCAGTTTGATAGAATA 252  
 DB 8443 TAGTGTGTTGTTGGGATAGGATAGGAGGATGAAA 8480  
  
 Search completed: May 27, 2004, 01:10:54  
 Job time : 299.637 secs





LOCATION: 1797..1850  
j-08-617-860B-32  
Query Match 7.9%; Score 46.6; DB 3; Length 1850;  
Best Local Similarity 44.8%; Pred. No. 0.037; Indels 0; Gaps 0;  
Matches 178; Conservative 0; Mismatches 219;  
153 TGTGTACATATTTTCCACAAATGTTATATATATAGTGTGTTGACAGGATGCAATC 212  
182 TATTGAAATATTTTGGAAATTTTAAATATATTTTAAATTTTAAATATATTTTAAATTC 241  
213 TTTTCTGCTTAAGGCTGCTGAGTTTAAATATATATATATATATATATATATATATATAT 272  
242 TTTTAAATATATATTTTAAAT 301  
273 GTAGTGGAGTTTATTTTAACTTTTAAATATATATATATATATATATATATATATATATAT 332  
302 AAATATAGTTTATTTTAAAT 361  
333 GTAGTTTATATATATCGCTTATATTTCCCATGAGTATGACATGACATTTAATTC 392  
362 AAATATATATTTTAAAGTTTATATATATTTTGAATTTTGAATATATGAAAAATTTTG 421  
393 TGTGTGCTGCCATGCTTCTTTTAACTTTTAAATATATATATATATATATATATATATATAT 452  
422 TTGGAGATATACCGAGATTTTAT 481  
453 TGATAATAGTTTATATAGTGTACTGCTGTAATGATGCTAAATATATATATATATATATATAT 512  
482 GTCCATTTGCTTTAAACCAACGAGTGTCTGACAAATGATTAACGATCTATGGAT 541  
513 TAAGGCTTACAGACATGTTTGAACATTTTTPACTT 549  
542 GAAAGTTTARGAGCAACGAGCTATTATTTTAAATTT 578

RESULT 4

S-08-605-106-4  
Sequence 4, Application US/08605106  
Patent No. 5910631  
GENERAL INFORMATION:  
APPLICANT: Topfer, R.  
APPLICANT: Martini, N.  
APPLICANT: Schell, J.  
TITLE OF INVENTION: MEDIUM CHAIN-SPECIFIC THIOESTERS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESS: Schwegman, Lundberg, Woessner & Kluth, P.A.  
STREET: P.O. Box 2938  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,106  
FILING DATE: 23-SEPT-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP94/02935  
FILING DATE: 01-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Woessner, Warren D  
REGISTRATION NUMBER: 30,440  
REFERENCE/DOCKET NUMBER: 235.001US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-373-6900  
TELEFAX: 612-339-3061  
TELEX:

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4098 Base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
MOLECULE TYPE: : DNS (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Cuphea lanceolata  
IMMEDIATE SOURCE:  
LIBRARY: genomic Lambda FIX II  
CLONE: C118g1  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1797..2294, 2658..2791, 2898..3011, 3132  
LOCATION: .3303, 3391..3459, 3672..3941)  
FEATURE:  
NAME/KEY: Startcodon  
LOCATION: 1797..1799  
FEATURE:  
NAME/KEY: exon II  
LOCATION: 1787..2294  
FEATURE:  
NAME/KEY: intron II  
LOCATION: 2295..2657  
FEATURE:  
NAME/KEY: exon III  
LOCATION: 2658..2791  
FEATURE:  
NAME/KEY: intron III  
LOCATION: 2792..2897  
FEATURE:  
NAME/KEY: exon IV  
LOCATION: 2898..3011  
FEATURE:  
NAME/KEY: intron IV  
LOCATION: 3012..3131  
FEATURE:  
NAME/KEY: exon V  
LOCATION: 3132..3303  
FEATURE:  
NAME/KEY: intron V  
LOCATION: 3304..3390  
FEATURE:  
NAME/KEY: exon VI  
LOCATION: 3391..3459  
FEATURE:  
NAME/KEY: intron VI  
LOCATION: 3460..3671  
FEATURE:  
NAME/KEY: exon VII  
LOCATION: 3672..3941  
FEATURE:  
NAME/KEY: Stopcodon  
LOCATION: 3942..3944  
US-08-605-106-4

Query Match 7.9%; Score 46.6; DB 2; Length 4098;  
Best Local Similarity 44.8%; Pred. No. 0.044; Indels 0; Gaps 0;  
Matches 178; Conservative 0; Mismatches 219;  
Qy 153 TGTGTACATATTTTCCACAAATGTTATATATATAGTGTGTTGACAGGATGCAATC 212  
Db 182 TATTGAAATATTTTGGAAATTTTAAATATATTTTAAATTTTAAATATATTTTAAATTC 241  
Qy 213 TTTTCTGCTTAAGGCTGCTGAGTTTAAATATATATATATATATATATATATATATATAT 272  
Db 242 TTTTAAATATATTTTAAAT 301  
Qy 273 GTAGTGGAGTTTATTTTAACTTTTAAATATATATATATATATATATATATATATATAT 332





QY	235	AGCTTAAAAA	AAAAACACCTTTCTCTT	CAATATGGCATCTAGT	GGAGTTTTTTTTTA	ACTTT	294
Db	1385	AAATTAACA	AGTTATCAAA	TTTTAAATTAATCATGAT	TCATATCTGTGTTTTT	CTTTT	1444
QY	295	AAAAACATCA	AAATTTGTTAAATCATTTG	TGTATCTAGT	AGTTTATTAATATCGGCTTA	354	
Db	1445	AAAAGATA	TAATTA	AAATCTT---TTATTAATTTATATAATTCATATAAGTAATGCTAA	1500		
QY	355	TATTTCCCAT	CGAATGATCAGAACTGACATTTAA	TTCACTTTTGTCGCCATGCTTCTT	414		
Db	1501	TAATTCAT	CTC	CACTATTTTCATTTAAATTTAAATTCACCAAGTAATTAATATAATTAAT	1560		
QY	415	TACTTTAA	CATATTTCTTTTGCAGAA	TGTAAGGTAATGATAATAGTATTTATATAAGTG	474		
Db	1561	GATTATAT	CTCGTTTATAAGAA	---TAA	TGTATTATGATTTTTTAAAGACAA	1616	
QY	475	TACTGGCTG	TAAATGATGCTTAATATAC	TTTAAGCAATTAAGGGCTTACAGAA	CATGCTTG	534	
Db	1617	AATCACTTT	A	GAAGTCTCTTTTAAATTTTCAATTAAGATTAAGAAATTTTTAT	1676		
QY	535	AAACTTTTTT	ACTTTTTATTGGGA	TAAAGAA	566		
Db	1677	TGTC	TTCTTTTTTAA	TTTTTTGTAATGAGCAA	1708		

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RESULT 10
US-09-543-681A-3626/c
; Sequence 3626, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETTON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543.681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 3626
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Proteus mirabilis
; US-09-543-681A-3626

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Query Match	7.5%	Score 44.6	DB 4	Length 237
Best Local Similarity	51.2%	Pred. No. 0.071		
Matches 104	Conservative 0	Mismatches 99	Indels 0	Gaps 0
QY	145	TAAGTTTCGTGTACATATTTTCCACAAATGTTATATTTATATAGTGTGGTTGAACAGG	204	
DB	210	TAATTTTCTATTTATATATATGATATTTAAATTTATTTCTATTTGTAATTTTTTAGATAAA	151	
QY	205	ATGCAATCTTTTGTTGTCATAAGGTGTCGAGTTTAAAAAACAACCTTTTCTTTTCAA	264	
DB	150	ATPACTATATTTATATATCTACCAAGGACTGTATAAAAAACAAGTGTGATCATATAGTGTAT	91	
QY	265	TATGCATGTGTAGTGAGTTTTTTTTTAACTTTTAAAAACATCAAAAATTTGTTAAAAATCATTTGT	324	
DB	90	TTTAGAAGAGATAAACAGGATGTTTTATATGCAAAAATATCAAAAATTAATGGGAAGCCTGGG	31	
QY	325	GTATATCTAGTAGTTTATAATTTAT	347	
DB	30	GCTCATGGGTTGTAAATAATAAT	8	

RESULT 11  
US-08-487-826B-13/c  
; Sequence 13, Application US/08487826B  
; Patent No. 5993827  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Kim L.  
; APPLICANT: Chitnis, Chetan

```

; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Pacenlin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; INFORMATION FOR SEQ ID NO: 13:
; LENGTH: 19124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
US-08-487-826B-13

Query Match          7.5%; Score 44.6; DB 2; Length 19124;
Best Local Similarity 46.0%; Pred. No. 0.18;
Matches 188; Conservative 0; Mismatches 219; Indels 2; Gaps 1;

QY      143   TTTATGTTCTGGTGTCACATAATTCCACAAGTGTATTAATTTATATAGTCTGGTTGAACA 202
DB      15936  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
           TTTTTTATTAATTAATAAATTTTTTATTTATTTATTTTATTTTATTAATTAATTTTTTT 15837

QY      203   GGATGCCAACTTTTGTTGTCTAAAGGCTCGCACGTTAAAAAAAACCAACCCTTTCTTTTC 262
DB      15836  ATTTATTTATTTTTTTTTTTATTTAAATAAAATTTTTTTTTTATTTATGATATATTTTTTTT 15777

QY      263   AATATGCCATGTAGTCGGAGCTTTTTTTTAACTTTTAAAAACATCAAAAATCTGTTAAATCAT 322
DB      15776  AACATTTTATTTTTTTTTTTTATTTATGATATATTTTTTATTTATATATATTTTTTT 15717

QY      323   GTGTATCTAGTAGTTTATAAATATCGGCTTATATTCCGCCATGAAATGATCAGAAGTGCAC 382
DB      15716  CTTTTTTTTTTTGTTTTATGATATATATTTTTTTTTTTTAAATGTTTTTTTTTTTCT--T 15659

QY      383   ATTTAAATTCATGTTTCTCGCGCATGTCCTTTACTTTTAAACATATTCCTTTTCGAGAATG 442
DB      15658  CTTTGTGTTTTTATTTTTTTTATAAACATTTTTTTTTTATATAAAATTTTTTTTAAATTT 15599

QY      443   TAAAGGTATGTAATATAGTTTATATTAAGTGACTCGGCTGTAATCATGCTAAATATAC 502
DB      15598  TTPTTGATAATCTTTTTCATTTTTTTTATCTATCAAAATTTATATTTTATATAATTTTA 15539

QY      503   TTATGCAATTAAGGGCTTACAGAACATGTTGAACCTTTTTTTTACTTTTT 551
DB      15538  TATTTTTTTAAAAAATTTTTTCTCCCTTTTTTTTTTTTTTTTTTTTTTTTATTT 15490

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RESULT 13  
US-10-204-708-14  
; Sequence 14, Application US/10204708

RESULT 14  
US-09-621-976-2813/C  
/ Sequence 2813, Application US/09621976  
/ Patent No. 6639063  
/ GENERAL INFORMATION:  
/ APPLICANT: Dumas Belne Edwards, J.B.  
/ APPLICANT: Jubesit, S.  
/ APPLICANT: Giordano, J.Y.  
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins  
/ FILE REFERENCE: GENSET.054PR2  
/ CURRENT APPLICATION NUMBER: US/09/621,976





GenCore version 5.1.6  
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1 nucleic - nucleic search, using sw model

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(without alignments)  
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effect score: 593  
sequence: 1 acattttatgtttacagctt.....acctccacattttattgctt 593

scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

sarched: 2953838 seqs, 2272363821 residues

total number of hits satisfying chosen parameters: 5907676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubna/US05\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubna/US07\_NEW\_PUB.seq:\*
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- 8: /cgn2\_6/ptodata/1/pubna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubna/US09A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubna/US10\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	593	100.0	1317	9	US-09-764-846-39
2	593	100.0	1317	15	US-10-091-483-39
3	579.2	97.7	1387	9	US-09-764-846-113
4	579.2	97.7	1387	15	US-10-091-483-113
5	578	97.5	1709	16	US-10-104-047-51
6	277.2	46.7	307	9	US-09-796-692-5699
7	277.2	46.7	307	15	US-10-040-862-5699
8	277.2	46.7	307	16	US-10-057-475B-5699
9	277.2	46.7	307	16	US-10-154-894B-5699
10	56.6	9.5	11691	15	US-10-312-841-2
11	56.6	9.5	3673778	15	US-10-311-455-2214
12	55	9.3	13038	15	US-10-311-455-1247
13	54.8	9.2	15387	15	US-10-311-455-157
14	54.4	9.2	7918	17	US-10-610-351A-15

15	54.4	9.2	13574	15	US-10-311-455-1289	Sequence 1289, Ap
16	54	9.1	3673778	15	US-10-312-841-1	Sequence 1, Appl
17	52.8	8.9	17848	15	US-10-239-676-28	Sequence 28, Appl
18	52.8	8.9	17848	15	US-10-240-453-38	Sequence 38, Appl
19	52.8	8.9	17848	17	US-10-257-166-58	Sequence 58, Appl
20	52.8	8.9	19087	15	US-10-311-455-765	Sequence 765, Ap
21	52.2	8.8	3855	13	US-10-282-122A-40650	Sequence 40650, A
22	51.6	8.7	8237	13	US-10-221-714A-528	Sequence 528, Ap
23	51.4	8.7	18512	13	US-10-311-455-949	Sequence 949, Ap
24	51.2	8.6	9652	15	US-10-311-455-1571	Sequence 1571, Ap
25	51	8.6	9652	15	US-10-311-455-881	Sequence 881, Ap
26	51	8.6	11805	15	US-10-311-455-1721	Sequence 1721, Ap
27	50.8	8.6	15872	13	US-10-221-714A-241	Sequence 241, Ap
28	50.6	8.5	4503	15	US-10-311-455-744	Sequence 744, Ap
29	50.6	8.5	8169	13	US-10-221-714A-9	Sequence 9, Appl
30	50.4	8.5	6294	15	US-10-311-455-1027	Sequence 1027, Ap
31	50.2	8.5	5424	15	US-10-311-455-827	Sequence 827, Ap
32	50.2	8.5	6038	15	US-10-311-455-38	Sequence 38, Appl
33	50.2	8.5	6101	13	US-10-221-613-10	Sequence 10, Appl
34	50	8.4	50	16	US-10-131-827-768	Sequence 768, Appl
35	50	8.4	50	15	US-10-131-827-7949	Sequence 7949, Ap
36	50	8.4	17419	15	US-10-239-676-100	Sequence 100, Ap
37	50	8.4	17419	15	US-10-311-455-1268	Sequence 1268, Ap
38	50	8.4	17419	15	US-10-240-453-112	Sequence 112, Ap
39	50	8.4	20486	15	US-10-240-485-164	Sequence 164, Ap
40	49.8	8.4	6112	15	US-10-311-455-462	Sequence 462, Ap
41	49.8	8.4	8423	15	US-10-311-455-1380	Sequence 1380, Ap
42	49.6	8.4	5557	15	US-10-311-455-1519	Sequence 1519, Ap
43	48.8	8.2	5888	15	US-10-240-485-10	Sequence 10, Appl
44	48.6	8.2	6109	13	US-10-221-613-33	Sequence 33, Appl
45	48.6	8.2	6109	15	US-10-311-455-299	Sequence 299, Ap

ALIGNMENTS

RESULT 1

US-09-764-846-39  
; Sequence 39, Application US/09764846  
; Patent No. US20020102638A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PTZ12  
; CURRENT APPLICATION NUMBER: US/09/764,846  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 348  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 39  
; LENGTH: 1317  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-846-39

Query Match	100.0%	Score	593	DB	9	Length	1317
Best Local Similarity	100.0%	Pred. No.	4e-115				
Matches	593	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	ACATCTTATGTTTACAGGCTTCCTCTTTGATGAAGATAGCAACGAAACTCAAAATGGT	60				
Db	629	ACATCTTATGTTTACAGGCTTCCTCTTTGATGAAGATAGCAACGAAACTCAAAATGGT	688				
Qy	61	GGCAGTCTTATACCACTGTTAGTATGTTTCGGAACCTGTTCCAGACACACTT	120				
Db	689	GGCAGTCTTATACCACTGTTAGTATGTTTCGGAACCTGTTCCAGACACACTT	748				
Qy	121	TATTAAGTGTAGAACACTTGTCTTTATGTTTGTGTATCATATTTCCAAATGTTATA	180				
Db	749	TATTAAGTGTAGAACACTTGTCTTTATGTTTGTGTATCATATTTCCAAATGTTATA	808				
Qy	181	ATTATATAGTGTGGTTGAACAGGATGCACTTTTGTGTCTTAAGGTGTCGAGTTAA	240				

Db 809 ATTTATATAGTGTGTTGAAACAGGATGCAATCTTTTGTGTCTAAAGGTGCTGCAGTTAA 868  
Qy 241 AAAAAAACAACCTTTCTTTCAATATGCGATGTAGTGGAGTTTTTTTAACTTTAAAAAC 300  
Db 869 AAAAAAACAACCTTTCTTTCAATATGCGATGTAGTGGAGTTTTTTTAACTTTAAAAAC 928  
Qy 301 ATCAAAAATTGTTAAATCAATTTGTTTAACTAGTGTATTAATATCGGCTTATATTC 360  
Db 929 ATCAAAAATTGTTAAATCAATTTGTTTAACTAGTGTATTAATATCGGCTTATATTC 988  
Qy 361 CCATGAATGATCAGAACTGCAATTTAATTCATGTTTGTCTCGCCAGCTTCTTTACTTT 420  
Db 989 CCATGAATGATCAGAACTGCAATTTAATTCATGTTTGTCTCGCCAGCTTCTTTACTTT 1048  
Qy 421 AACATATTTCTTTTGCAGAACTGCAATTTAATTCATGTTTGTCTCGCCAGCTTCTTTACTTT 480  
Db 1049 AACATATTTCTTTTGCAGAACTGCAATTTAATTCATGTTTGTCTCGCCAGCTTCTTTACTTT 1108  
Qy 481 CTGTAATGATGCTAAATATATCTTTTATGCAATTAAGGCTTACAGAACATGTTGAAACTT 540  
Db 1109 CTGTAATGATGCTAAATATATCTTTTATGCAATTAAGGCTTACAGAACATGTTGAAACTT 1168  
Qy 541 TTTTACTTTTATGCGAATAGGAATGTTTGCACCTCCACATTTTATGCTT 593  
Db 1169 TTTTACTTTTATGCGAATAGGAATGTTTGCACCTCCACATTTTATGCTT 1221

RESULT 2  
US-10-091-483-39  
; Sequence 39, Application US/10091483  
; Publication No. US20030049650A1  
; GENERAL INFORMATION:  
; APPLICANT: rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT212C1  
; CURRENT APPLICATION NUMBER: US/10/091,483  
; CURRENT FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 348  
; Prior application removed - See File Wrapper or Palm  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 39  
; LENGTH: 1317  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-091-483-39

Query Match 100.0%; Score 593; DB 15; Length 1317;  
Best Local Similarity 100.0%; Pred. No. 4e-115;  
Matches 593; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACATCTTATGTTTACAGGCTTCTGTTGATGAAGATAGCAACGGAACCTCAAAATGGT 60  
Db 629 ACACTTATGTTTACAGGCTTCTGTTGATGAAGATAGCAACGGAACCTCAAAATGGT 688  
Qy 61 GGAGTCTTATPACAGTGTAGTATGTTTCTGGAACCTGCTTGCAGACACATTT 120  
Db 689 GGCAGTCTTATPACAGTGTAGTATGTTTCTGGAACCTGCTTGCAGACACATTT 748  
Qy 121 TATTAAGTGTAGAACACTTCTTATGTTTGTGTTACATATTTTCCACAAATGTTATA 180  
Db 749 TATTAAGTGTAGAACACTTCTTATGTTTGTGTTACATATTTTCCACAAATGTTATA 808  
Qy 181 ATTTATATAGTGTGTTGAACAGGATGCAATCTTTTGTGTTCTAAAGGTGCTGCAGTTAA 240  
Db 809 ATTTATATAGTGTGTTGAACAGGATGCAATCTTTTGTGTTCTAAAGGTGCTGCAGTTAA 868  
Qy 241 AAAAAAACAACCTTTCTTTCAATATGCGATGTAGTGGAGTTTTTTTAACTTTAAAAAC 300  
Db 869 AAAAAAACAACCTTTCTTTCAATATGCGATGTAGTGGAGTTTTTTTAACTTTAAAAAC 928  
Qy 301 ATCAAAAATTGTTAAATCAATTTGTTTAACTAGTGTATTAATATCGGCTTATATTC 360  
Db 929 ATCAAAAATTGTTAAATCAATTTGTTTAACTAGTGTATTAATATCGGCTTATATTC 988

## RESULT 3

US-09-764-846-113  
; Sequence 113, Application US/09764846  
; Patent No. US20020102638A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT212  
; CURRENT APPLICATION NUMBER: US/09/764,846  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 348  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 113  
; LENGTH: 1387  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (23)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (104)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (739)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (1378)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (1386)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-764-846-113

Query Match 97.7%; Score 579.2; DB 9; Length 1387;  
Best Local Similarity 99.3%; Pred. No. 3.3e-112;  
Matches 589; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 ACATCTTATGTTTACAGGCTTCTGTTTGTGATGAAGATAGCAACGGAACCTCAAAATGGT 60  
Db 620 ACACTTATGTTTACAGGCTTCTGTTTGTGATGAAGATAGCAACGGAACCTCAAAATGGT 679  
Qy 61 GGCAGTCTTATPACAGTGTAGTATGTTTCTGGAACCTGCTTGCAGACACATTT 120  
Db 680 GGCAGTCTTATPACAGTGTAGTATGTTTCTGGAACCTGCTTGCAGACACATTT 738  
Qy 121 TATTAAGTGTAGAACACTTCTTATGTTTGTGTTACATATTTTCCACAAATGTTATA 180  
Db 739 NATTAAGTGTAGAACACTTCTTATGTTTGTGTTACATATTTTCCACAAATGTTATA 798  
Qy 181 ATTTATATAGTGTGTTGAACAGGATGCAATCTTTTGTGTTCTAAAGGTGCTGCAGTTAA 240  
Db 799 ATTTATATAGTGTGTTGAACAGGATGCAATCTTTTGTGTTCTAAAGGTGCTGCAGTTAA 858

241 AAAAAAAAAAAGCTTTCTTCAATATGCGATGTAGTGGAGTTTAACTTTAAAAAC 300  
859 AAAAAAAAAAAGCTTTCTTCAATATGCGATGTAGTGGAGTTTAACTTTAAAAAC 918  
301 ATCAAAATTTGTAATAATCAATGTGTATCTAGTATGTTTAAATATCGGCTTATATTC 360  
919 ATCAAAATTTGTAATAATCAATGTGTATCTAGTATGTTTAAATATCGGCTTATATTC 978  
361 CCATGAATGATCAGAACTGACATTTAATTCATGTTCTCGCCATGCTTCTTACTTT 420  
979 CCATGAATGATCAGAACTGACATTTAATTCATGTTCTCGCCATGCTTCTTACTTT 1038  
421 AACATATTTCTTTTGCAGAACTGATAAGGTAATGATAATGTTTATATAAGTGTACTGG 480  
1039 AACATATTTCTTTTGCAGAACTGATAAGGTAATGATAATGTTTATATAAGTGTACTGG 1098  
481 CTGTAATGATGATAATGATAATGATAATGATAATGATAATGATAATGATAATGATAATG 540  
1099 CTGTAATGATGATAATGATAATGATAATGATAATGATAATGATAATGATAATGATAATG 1158  
541 TTTTACTTTTATGGAATAGGAATGTTTGCACCTCCACATTTTATGCTT 593  
1159 TTTTACTTTTATGGAATAGGAATGTTTGCACCTCCACATTTTATGCTT 1211

RESULT 4  
S-10-091-483-113  
Sequence 113, Application US/10091483  
Publication No. US20030049650A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: FTZ12C1  
CURRENT APPLICATION NUMBER: US/10/091,483  
CURRENT FILING DATE: 2002-03-07  
NUMBER OF SEQ ID NOS: 348  
Prior Application removed - See File Wrapper or Palm  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 113  
LENGTH: 1387  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (23)  
OTHER INFORMATION: n equals a.t.g, or c  
NAME/KEY: misc\_feature  
LOCATION: (104)  
OTHER INFORMATION: n equals a.t.g, or c  
NAME/KEY: misc\_feature  
LOCATION: (739)  
OTHER INFORMATION: n equals a.t.g, or c  
NAME/KEY: misc\_feature  
LOCATION: (1378)  
OTHER INFORMATION: n equals a.t.g, or c  
NAME/KEY: misc\_feature  
LOCATION: (1386)  
OTHER INFORMATION: n equals a.t.g, or c

Query Match 97.7%; Score 579.2; DB 15; Length 1387;  
Best Local Similarity 99.3%; Pred. No. 3.3e-112;  
Matches 589; Conservative 2; Mismatches 1; Indels 1; Gaps 1;  
1 ACATCTTATGTTTACAGGCTTCCTGTTTATGATGAAGATAGCAACGGAATACTCAAAATGCT 60  
620 ACATCTTATGTTTACAGGCTTCCTGTTTATGATGAAGATAGCAACGGAATACTCAAAATGCT 679  
61 GCGAGTCTTATTAACAGTGTGTAGTATGTTTCTGGAATGCTTGCACGCAACATTT 120  
680 GCGAGTCTTATTAACAGTGTGTAGTATGTTTCTGGAATGCTTGCACGCAACATTT 738  
121 TATTAACGTGTAGAACACTGCTTATGTTTGTGTACATATTTCCACAAATGTTTATA 180

Db 739 NATTAACGTGTAGAACACTGCTTATGTTTGTGTACATATTTCCACAAATGTTTATA 798  
Qy 181 ATTTATATAGTGTGTTTCAACAGATGCAATCTTTTGTGTCTAAAGGTGCTGCAGTTAA 240  
Db 799 ATTTATATAGTGTGTTTCAACAGATGCAATCTTTTGTGTCTAAAGGTGCTGCAGTTAA 858  
Qy 241 AAAAAAACAACCTTTCTTCAATATGCGATGTAGTGGAGTTTAACTTTAAAAAC 300  
Db 859 AAAAAAACAACCTTTCTTCAATATGCGATGTAGTGGAGTTTAACTTTAAAAAC 918  
Qy 301 ATCAAAATTTGTAATAATCAATGTGTATCTAGTATGTTTAAATATCGGCTTATATTC 360  
Db 919 ATCAAAATTTGTAATAATCAATGTGTATCTAGTATGTTTAAATATCGGCTTATATTC 978  
Qy 361 CCCATGAATGATCAGAACTGACATTTAATTCATGTTCTCGCCATGCTTCTTACTTT 420  
Db 979 CCCATGAATGATCAGAACTGACATTTAATTCATGTTCTCGCCATGCTTCTTACTTT 1038  
Qy 421 AACATATTTCTTTTGCAGAACTGATAAGGTAATGATAATGTTTATATAAGTGTACTGG 480  
Db 1039 AACATATTTCTTTTGCAGAACTGATAAGGTAATGATAATGTTTATATAAGTGTACTGG 1098  
Qy 481 CTGTAATGATGATAATGATAATGATAATGATAATGATAATGATAATGATAATGATAATG 540  
Db 1099 CTGTAATGATGATAATGATAATGATAATGATAATGATAATGATAATGATAATGATAATG 1158  
Qy 541 TTTTACTTTTATGGAATAGGAATGTTTGCACCTCCACATTTTATGCTT 593  
Db 1159 TTTTACTTTTATGGAATAGGAATGTTTGCACCTCCACATTTTATGCTT 1211

RESULT 5  
US-10-104-047-51  
Sequence 51, Application US/10104047  
Publication No. US20030236392A1  
GENERAL INFORMATION:  
APPLICANT: HELIX RESEARCH INSTITUTE  
TITLE OF INVENTION: No. US20030236392A1el full length cdna  
FILE REFERENCE: H1-A0105  
CURRENT APPLICATION NUMBER: US/10/104,047  
CURRENT FILING DATE: 2002-03-25  
PRIOR APPLICATION NUMBER:  
PRIOR FILING DATE:  
NUMBER OF SEQ ID NOS: 4096  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 51  
LENGTH: 1709  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-104-047-51

Query Match 97.5%; Score 578; DB 16; Length 1709;  
Best Local Similarity 100.0%; Pred. No. 6.4e-112;  
Matches 578; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 16 AGGCTTCCTGTTTATGATGAAGATAGCAACGGAATACTCAAAATGTTGCGCAGTTCTTATTAC 75  
Db 1056 AGGCTTCCTGTTTATGATGAAGATAGCAACGGAATACTCAAAATGTTGCGCAGTTCTTATTAC 1115  
Qy 76 CAGTTGTAGTATGTTTCTGGAACCTGCTTCCAGACACATTTATTAACTGTTAGAA 135  
Db 1116 CAGTTGTAGTATGTTTCTGGAACCTGCTTCCAGACACATTTATTAACTGTTAGAA 1175  
Qy 136 CACTTGTCTTATGTTGTGTACATATTTTCCACAAATGTTTATATAATGATAGTGG 195  
Db 1176 CACTTGTCTTATGTTGTGTACATATTTTCCACAAATGTTTATATAATGATAGTGG 1235  
Qy 196 TTGACAGGATGCAATCTTTTGTGTCTAAAGGTGCTGCAGTTTAAAAAACAACCTT 255  
Db 1236 TTGACAGGATGCAATCTTTTGTGTCTAAAGGTGCTGCAGTTTAAAAAACAACCTT 1295  
Qy 256 TTCTTTCAATATGCCATGTAGTGGAGTTTCTTAACTTTAAAAACATCAAAATGTTTAA 315

Db 1296 TTCTTTCAATATGCGCATGATGAGTGTGTTTAACTTTTAAACATCAAAATTTGTAA 1355  
Qy 316 AATCATTTGTTATCTAGTAGTTTAAATATATCGGCTTATATTTCCCATGAATGATCAG 375  
Db 1356 AATCATTTGTTATCTAGTAGTTTAAATATATCGGCTTATATTTCCCATGAATGATCAG 1415  
Qy 376 AACTGACATTTAATTCATGTTTGTCTCGCCATGCTTCTTTACTTTAAATATTTCTTTTG 435  
Db 1416 AACTGACATTTAATTCATGTTTGTCTCGCCATGCTTCTTTACTTTAAATATTTCTTTTG 1475  
Qy 436 CACAATGTAAGTAATGATTAATGATTTATATAGTGTACTGCTCTAAATGATGCTA 495  
Db 1476 CACAATGTAAGTAATGATTAATGATTTATATAGTGTACTGCTCTAAATGATGCTA 1535  
Qy 496 AATATATCTTTATGCAATTAAGGCTTTACAGACATGTTGAACTTTTACTTTTATTTG 555  
Db 1536 AATATATCTTTATGCAATTAAGGCTTTACAGACATGTTGAACTTTTACTTTTATTTG 1595  
Qy 556 GGAATAGGAATGTTTGCACCTCCACATTTTATGCTT 593  
Db 1596 GGAATAGGAATGTTTGCACCTCCACATTTTATGCTT 1633

RESULT 6  
US-09-796-692-5699/c  
; Sequence 5699, Application US/09796692  
; Publication No. US20020198362A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Mannion, Jane  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY  
; FILE REFERENCE: 2077.001200  
; CURRENT APPLICATION NUMBER: US/09/796,692  
; PRIOR FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/200,779  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 60/223,416  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; NUMBER OF SEQ ID NOS: 9997  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5699  
; LENGTH: 307  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-796-692-5699

Query Match 46.7%; Score 277.2; DB 9; Length 307;  
Best Local Similarity 98.6%; Pred. No. 7.4e-49;  
Matches 290; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 ACATCTTATGTTTACAGGCTTCCTGTTTGATGATAGATGCAACGGAACCTCAAAATGGT 60  
Db 293 ACATCTTATGTTTACAGGCTTCCTGTTTGATGATAGATGCAACGGAACCTCAAAATGGT 234  
Qy 61 GGCAGTCTTATTTACACAGTCTGTTAGTATTTGTTCTGGAACCTGCTTCCCAAGACAACTT 120  
Db 233 GGCAGTCTTATTTACACAGTCTGTTAGTATTTGTTCTGGAACCTGCTTCCCAAGACAACT 174  
Qy 121 TATTAACTGTTAGAACACTTCTGCTTTATGTTTGTGTGTACATATTTTCCCAAAATGTTATA 180  
Db 173 TATTAACTGTTAGAACACTTCTGCTTTATGTTTGTGTGTACATATTTTCCCAAAATGTTATA 114  
Qy 181 ATTATATAGTGTGTTTCAACAGGATGCAATCTTTTGTGTCTAAAGTGCTGCTGAGTTAA 240  
Db 113 ATTATATAGTGTGTTTCAACAGGATGCAATCTTTTGTGTCTAAAGTGCTGCTGAGTT-A 55  
Qy 241 AAAAAAACAACCTTTCTTCAATATGCGCATGATGCGAGTGTGTTTAACTTT 294  
Db 54 AAAAAAACAACCTTTCTTCAATATGCGCATGATGCGAGTGTGTTTAACTTT 1

RESULT 7  
US-10-040-862-5699/c  
; Sequence 5699, Application US/10040862  
; Publication No. US20030078396A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Mannion, Jane  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Hematological Malignancies  
; FILE REFERENCE: 014058-013520US  
; CURRENT APPLICATION NUMBER: US/10/040,862  
; PRIOR FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: US 60/223,416  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: US 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: US 09/796,692  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 10467  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5699  
; LENGTH: 307  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-040-862-5699

Query Match 46.7%; Score 277.2; DB 15; Length 307;  
Best Local Similarity 98.6%; Pred. No. 7.4e-49;  
Matches 290; Conservative 0; Mismatches 3; Indels 1; Gaps 1;







RESULT 12  
S-10-311-455-1247  
Sequence 1247, Application US/10311455  
Publication No. US20030143606A1  
GENERAL INFORMATION:  
APPLICANT: OLEK, Alexander  
APPLICANT: BERLIN, Kurt  
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation  
FILE REFERENCE: 5013.1014  
CURRENT APPLICATION NUMBER: US/10/311,455  
CURRENT FILING DATE: 2002-12-16  
PRIOR APPLICATION NUMBER: PCT/EP01/07537  
PRIOR FILING DATE: 2001-07-02  
PRIOR APPLICATION NUMBER: DE 10032529.7  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: DE 10043826.1  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 2424  
SEQ ID NO 1247  
LENGTH: 13038  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
S-10-311-455-1247  
Query Match 9.3%; Score 55; DB 15; Length 13038;  
Best Local Similarity 52.4%; Pred. NO. 0.25;  
Matches 144; Conservative 1; Gaps 1;  
Y 77 AGTGTGATGTTGTTCTCGGAACCTGTCGACAGACACATTTATTAACTGTTAGA-A 135  
b 4440 ATTTTGTGTAATAGATGGAAGGTTTAAATGAGATTAATTAATGTTTGTAGT 4499  
Y 136 CACTTGCTTTATGTTGTTGATACATATTTCCACAAATGTTTATATTTATATAGTGG 195  
b 4500 TGAGTGGGTTTAAATTAATTAAGTTTATTTTAAATTTTGTAAATAGTTGATTTTA 4559  
Y 196 TTGAACAGGATGCAATCTTTTGTCTAAAGTGTGTCAGTTAAAGGACCAACCTT 255  
b 4560 TTAAGAGTGATGTTGTTTTTTTTTTTGTATTTGGTAAATATAAAGGATGAGTT 4619  
Y 256 TTCTTCAATATGCGATGATGAGTGGAGTTTCTTAACTTTAAAGACATCAAAATGTTAA 315  
b 4620 TTTTTCATTTTGTGTATAGTTGTTGTTATTTTATTTAGGAGGAGATGAGTTGAT 4679  
Y 316 AATCATGTTGTTATCTAGTAGTTTATAATATCGG 350  
b 4680 AATTATGTTGAGATATGAATATTTTGTTCGG 4714  
RESULT 13  
S-10-311-455-157  
Sequence 157, Application US/10311455  
Publication No. US20030143606A1  
GENERAL INFORMATION:  
APPLICANT: OLEK, Alexander  
APPLICANT: PIEPENBROCK, Christian  
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation  
FILE REFERENCE: 5013.1014  
CURRENT APPLICATION NUMBER: US/10/311,455  
CURRENT FILING DATE: 2002-12-16  
PRIOR APPLICATION NUMBER: PCT/EP01/07537  
PRIOR FILING DATE: 2001-07-02  
PRIOR APPLICATION NUMBER: DE 10032529.7  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: DE 10043826.1  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 2424

SEQ ID NO 157  
LENGTH: 15387  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-311-455-157  
Query Match 9.2%; Score 54.8; DB 15; Length 15387;  
Best Local Similarity 45.2%; Pred. NO. 0.3;  
Matches 238; Conservative 1; Gaps 1;  
Y 45 ABAACCTCAAAATGCTGGCAGTCTCTTATTACCAGTTGTTAGTATTGTTCTCGAAACTGCT 105  
b 9796 AGAATCGGAATTTGGGTGTTATTTTGTATTTTATTTTATTTTATTTTATTTTATTTT 9855  
Y 106 TGCCAAGACAAACATTTATTAACATGTTAGAACACCTGCTTTATGTTTGTGTACATATT 165  
b 9856 TTAGATATTAAAGTTTGTAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 9915  
Y 166 TCCACAAATGTTATTAATTTATATAGTGTGGTTGACAGATGCAATCTTTTGTGCTCAA 225  
b 9916 TTATTAGATATTAAAGTTTGTAAATTTTATTTTATTTTATTTTATTTTATTTTATTT 9975  
Y 226 AGGTGCTGCAGTTAAAAAACAACCTTTTCTTCAATATGCGATGATGAGGATTTT 285  
b 9976 TTTTATTAGATATTAAAGTTTGTAAATTTTATTTTATTTTATTTTATTTTATTTTATTT 10035  
Y 286 TTAACTTTAAAAACATCAAAATTTGTTAAATCATTTGTTATCTAGTACTATTAATT 345  
b 10036 ATTTTATTTATAGATATTAAAGTTTGTAAATTTTATTTTATTTTATTTTATTTTATTT 10095  
Y 346 ATCGGCTTATATTTCCCATGAATGATCAGAACTGACATTTAAATCATGTTTGTCTGCC 405  
b 10096 GTTATTTTATTTATAGATATTAAAGTTTGTAAATTTTATTTTATTTTATTTTATTTT 10155  
Y 406 ATGCTTCTTACTT-TAACAATATTTCTTTTGCAGATGTAAGTAAGTAATGATTAATTAGT 464  
b 10156 ATGTTATTTTATTTATAGATATTAAAGTTTGTAAATTTTATTTTATTTTATTTTATTT 10215  
Y 465 TATATAAGTGTACTGGCTGTAATGATGCTAAATATATCTTTATGCAATTAAGGGCTTACA 524  
b 10216 TTTATTTGTTATTTTATTTATAGATATTAAAGTTTGTAAATTTTATTTTATTTTATTT 10275  
Y 525 GAACATGTTGAACTTTTCTTTTATTTATTTGGAATAAGGAATGTT 570  
b 10276 GTATTTATTTGTTATTTTATTTATAGATATTAAAGTTTGTAAATTTT 10321  
RESULT 14  
US-10-610-351A-15  
Sequence 15, Application US/10610351A  
Publication No. US20040093632A1  
GENERAL INFORMATION:  
APPLICANT: DIXON, RICHARD A.  
APPLICANT: PAIVA, NANCY L.  
APPLICANT: XIE, DEYU  
APPLICANT: SHARMA, SHASHI  
TITLE OF INVENTION: GENETIC MANIPULATION OF CONDENSED TANNINS  
FILE REFERENCE: NELS:004US  
CURRENT APPLICATION NUMBER: US/10/610,351A  
CURRENT FILING DATE: 2003-06-30  
PRIOR APPLICATION NUMBER: 60/392,562  
PRIOR FILING DATE: 2002-06-28  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 7918  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-10-610-351A-15  
Query Match 9.2%; Score 54.4; DB 17; Length 7918;



Best Local Similarity 48.4%; Pred. No. 0.27;  
Matches 151; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

QY 86 TATTGTTCTGGAACAGCTGTCGCAAGCAACATTAATTAAGCTGTAGAACACATTCGCTTT 145  
Db 4288 TTTAAATTTGTTGTTTGTATTAATAAGCTAATAGTTTATAGCATTTTAATGAATATTC 4347

QY 146 ATGTTTGTGTTGATACATATTTTCCACAATGTTATTAATTTATATAGTGTGTTGAACAGGA 205  
Db 4348 AAGTTTCCGTTGTTTACATTTTGAAGAAATAAATATTAATATATTTCTGAAGATTTTGT 4407

QY 206 TGCAATCTTTTGTGTTCTAAAGTGCTGAGTTTAAAAAACAACCTTTTCTTTCAAT 265  
Db 4408 TTTTGTGTTAATCACTACATGACACAGTAAATAGAAAAAATCTATTTTGGAA 4467

QY 266 ATGCGATGAGTGGAGTTTATTTTAACTTTAAAAACATCAAAAATGTTTAAATCATTTGTG 325  
Db 4468 AAGTATGATCGGTGTTTAGAATACTTCCGAAATCAACCGCTATATTTCTAATCA 4527

QY 326 TTATCTAGTATTTATTAATTTATCGGCTTATATTTCCCATGAATCATCAGAACTGACATT 385  
Db 4528 CTATGTAATATTGTAACCAATGGGTAAACACTCAACTACAAACTTCTTAATTAATG 4587

QY 386 TAATTCATGTTT 397  
Db 4588 TCATTTTGTTT 4599

RESULT 15  
US-10-311-455-1289  
; Sequence 1289, Application US/10311455  
; Publication No. US20030143606A1  
; GENERAL INFORMATION:  
; APPLICANT: OLEK Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation  
; FILE OF INVENTION: cytosine methylation  
; FILE REFERENCE: 5013.1014  
; CURRENT APPLICATION NUMBER: US/10/311,455  
; PRIOR FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: PCT/EP01/07537  
; PRIOR FILING DATE: 2001-07-02  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 2424  
; SEQ ID NO 1289  
; LENGTH: 13574  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-311-455-1289

Query Match 9.2%; Score 54.4; DB 15; Length 13574;  
Best Local Similarity 48.0%; Pred. No. 0.34;  
Matches 191; Conservative 0; Mismatches 201; Indels 6; Gaps 1;

QY 163 TTTTCCAAATGTTATATATATAGTGTGTTGAACAGGATGCAATCTTTTGTGTC 222  
Db 3481 TTTTAGAAAATGTTAGATTTAAGTAGTGAAGCGTAAAGTTTTGTATTTGTAAGTT 3540

QY 223 TAAAGTGCTGCAAGTTAAAAAACAACCTTTCTTTCAATATGGCATGTAGTGGAGT 282  
Db 3541 GTTTGTTTTTAAATTAATAAATAAATAGGTTTAAATATATATTTTAAAAAATATTTT 3600

QY 283 TTTTAACTTTAAACATCAAAAATGTTAAATCATTTGTTATCTAGTAGTTTATA 342  
Db 3601 TGTAGGTTTTTTTAAAGAAAAAATTTTATAAATAATAGTAAGAAATTAAGTAATTTTA 3660

QY 343 ATTATCGGCTTATATTTCCCATGAATCATCAGAACTGACATTTAATTCATGTTTGTCTC 402

Db 3661 GTTAGTATAGAAAATAGTTAGATGAATGTCGAAAGAAATTTTATTTGAATATTGTTTG 3720  
QY 403 GCCA-----TGCCTTCTTACTTTAAACATATTTCTTTGCGAGAAATGTAAGAGGTAATGAT 456  
Db 3721 GTTTGATGTTTGGTATTAAATATTTTATTTTATTTATTTATAGTATTTTAGATATAGTTTG 3780  
QY 457 AATTAGTTTATATAAGTGTACTGGCTGTAAATGATGCTAAATATATCTTTATGCAATTAAAG 516  
Db 3781 TTTAAGTTTATGTTGTGTATATGTTGTATAGATATAAATATTTTGTTTATATAATATTA 3840  
QY 517 GCGTTACAGAACATGTTGAAACCTTTTCTTTTACTTTTATT 554  
Db 3841 TATTTTACGTGTGTGATATAAATTTTGGTATTATTTT 3878

Search completed: May 27, 2004, 01:11:02  
Job time : 442.232 secs